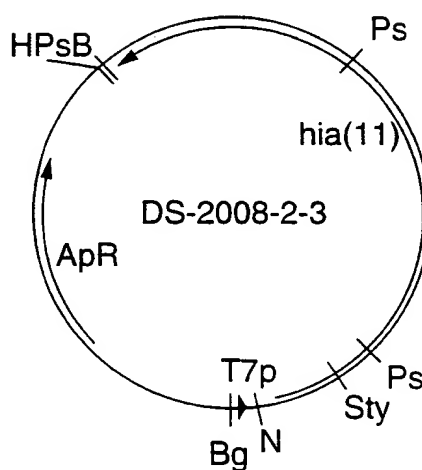


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Restriction map of DS-2008-2-3, pT7 hia (11).



pT7 hia (11)

FIG.1A

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FIG. 1B

FIG. 1B

Oligonucleotides used to PCR amplify the full-length strain 11 *hla* gene for expression studies.

sense

EcoR I Nde I

5' GCGAATTCATATGACAAATTTTAAACGTTATTGGAAT 3' M N K I F N V I W N P

SEQ ID NO:2
SEQ ID NO:1

5038.SL

antisense

5' AAAACAGCGGTTCAGCAGGTGTTGGTTACCACTGGTAATAG
3' TTTGTCCGCAACGTCACCAACCAATGGTCACATTATCTAAGCCCTAGCG

SEQ ID NO:5
SEQ ID NO:4
SEQ ID NO:3

5039.SL

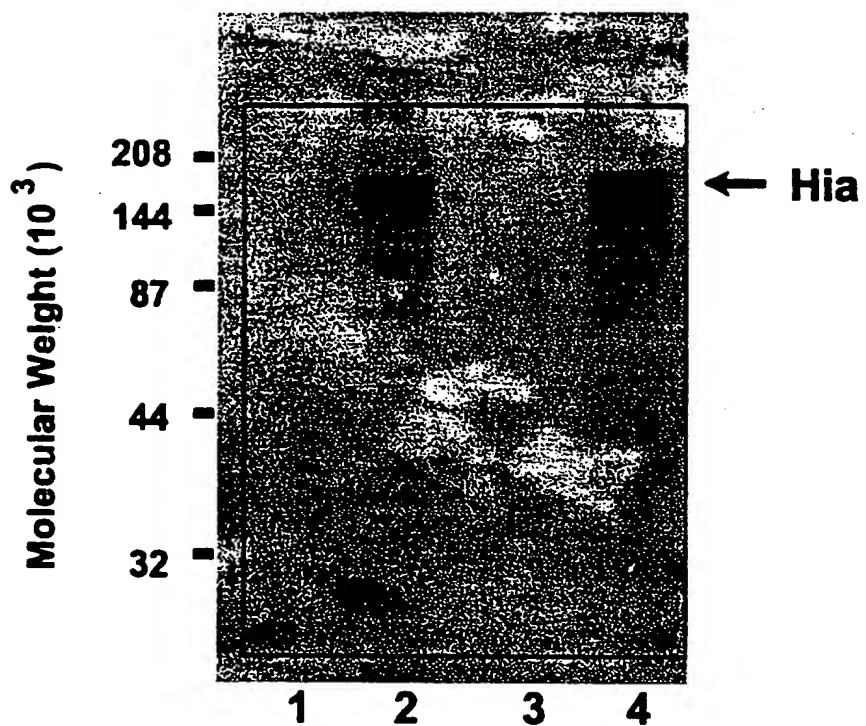
EcoR I BamH I

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FIG.2

FIG. 2



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Construction of DS-2092-1 and DS-2092-40,
plasmids containing tandem T7 hia (11) genes.

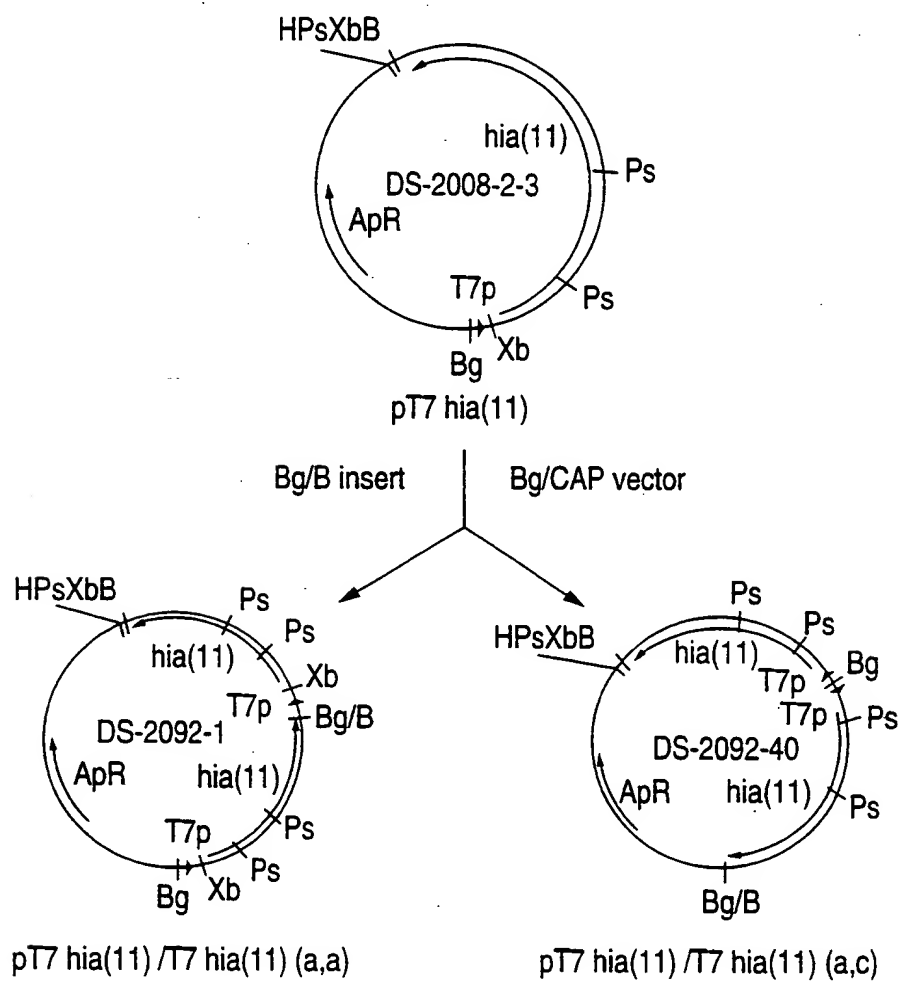


FIG.3

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FIG. 4

FIG.4

Sites for N-terminal truncations of rhia proteins.

MNKIFNVIMNVVITQIWVVSE²¹LIRTHHKCASAT³³VAVAV³⁸LATLLSATVEANAN⁵²TPVINKLKAYGD (SEQ ID NO.6)

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Construction of plasmids expressing truncated hia (11) genes.

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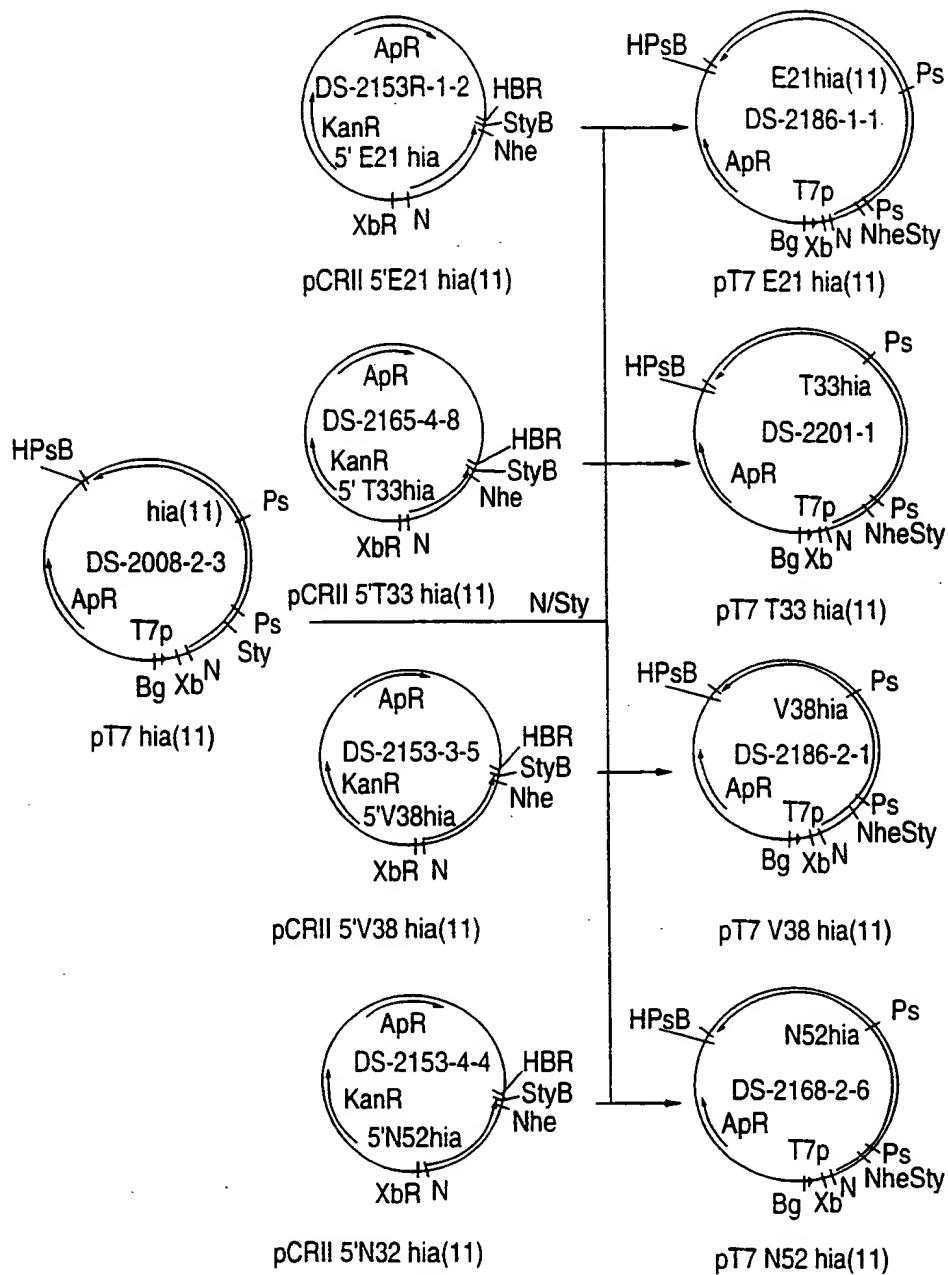


FIG.5A

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TOP SECRET

FIG.5B

Oligonucleotide primers to PCR amplify truncated strain 11 *hla* genes.

E21	EcoR I Nde I ↓ ↓				
		M E L T R T H T K C A			SEQ ID NO: 8
5'		GGGAATTCATATGGAACCTCACTCCACCCACACCAATGGGCC	3'	5524.SL	SEQ ID NO: 7
T33					
		M T V A V A V L A T L			SEQ ID NO: 10
5'		GGGAATTCATATGACCGTGGCGGTTCGGTATGGCAACCTG	3'	5525.SL	SEQ ID NO: 9
V38					
		M V L A T L L S A T			SEQ ID NO: 12
5'		GGGAATTCATATGTTATGGCAACCTGTGTCCGAACG	3'	5526.SL	SEQ ID NO: 11

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FIG. 5B

FIG. 5B'

N52
5' M N T P V T N K L K A 3' 5527.SL
GGGAATTCATATGAATACCTCTGTACGAATAAGTTGAAGCTT SEQ ID NO:14
SEQ ID NO:13

antisense

5' H T I T F A L A K D L G 3' SEQ ID NO:17
CACACCATTTACCTTTTGGCTAGCGAAGACCTTGGTGG
GTGTGTAATGGAACCGGATCGCTTCTGGAACCACTAGGCG 5' SEQ ID NO:16
5528.SL
Nhe I Sty I BamH I

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Construction of BK-96-2-11,
a plasmid containing T7 V38 hia(11) and cer.

09/936362, 12/15/94

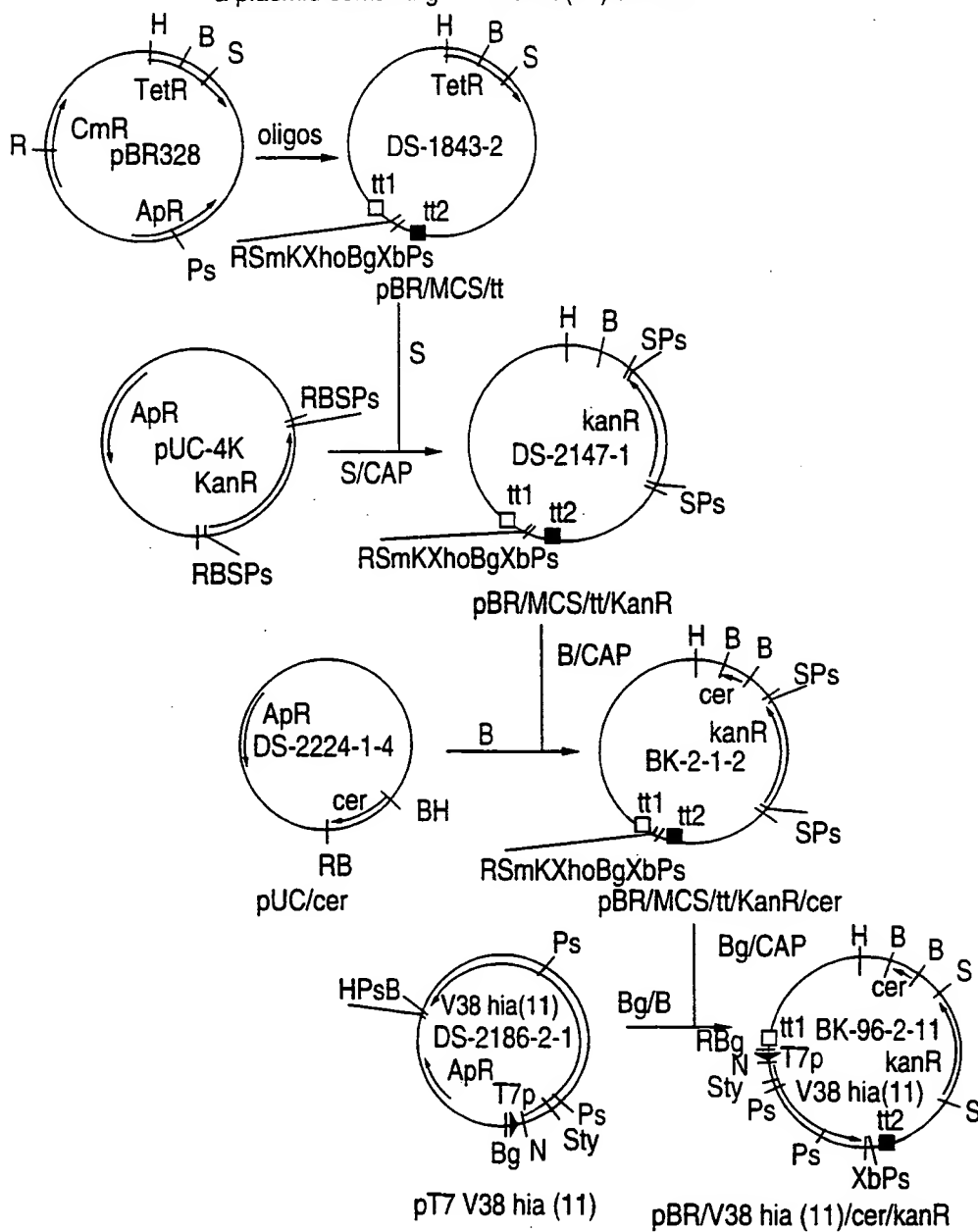


FIG.6A

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TOGETHER 29292929

FIG.6B

Oligonucleotides used to generate the multiple cloning site and transcription terminators for the expression plasmids

```

"R"      trpA terminator      R      Sn      KXho      Bg Xb      ...
AATTGCAGCCCGCCTAATGAGCGGCTTTTGAATTCOCGGTA  ↓↓  ↓  ↓  ↓  ...
CGTCGGCGGATTACTCGCCCGAAGAACTTAAAGGCGCCCATGAGCTCTAGAG  CCTCGAGATCTCTAGAC...
ATCTG...

... Ps      ↓  T7 gene 10 terminator
... TCCAGATATAGTTCTCTCTTCAGCAAAAACCCCTCAA

... ACGTCTATATCAAGGAGGAAGTCGTTTTTTCGGGAGTTCTGGCAATC

"Ps"
GACCCGTTTACAGCCCGCCCAAGCGGTTATGCTAGTTATTGCTCAGCGGTGGCAGCAGCGTCCA
TCCGGGGTTCCCAATACCATCAATAACGAGTGGCCACCGTGTGGC

```

SEQ ID NO: 50
SEQ ID NO: 51

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Construction of DS-2242-1 and DS-242-2,
plasmids containing T7 hia (33) and cer.

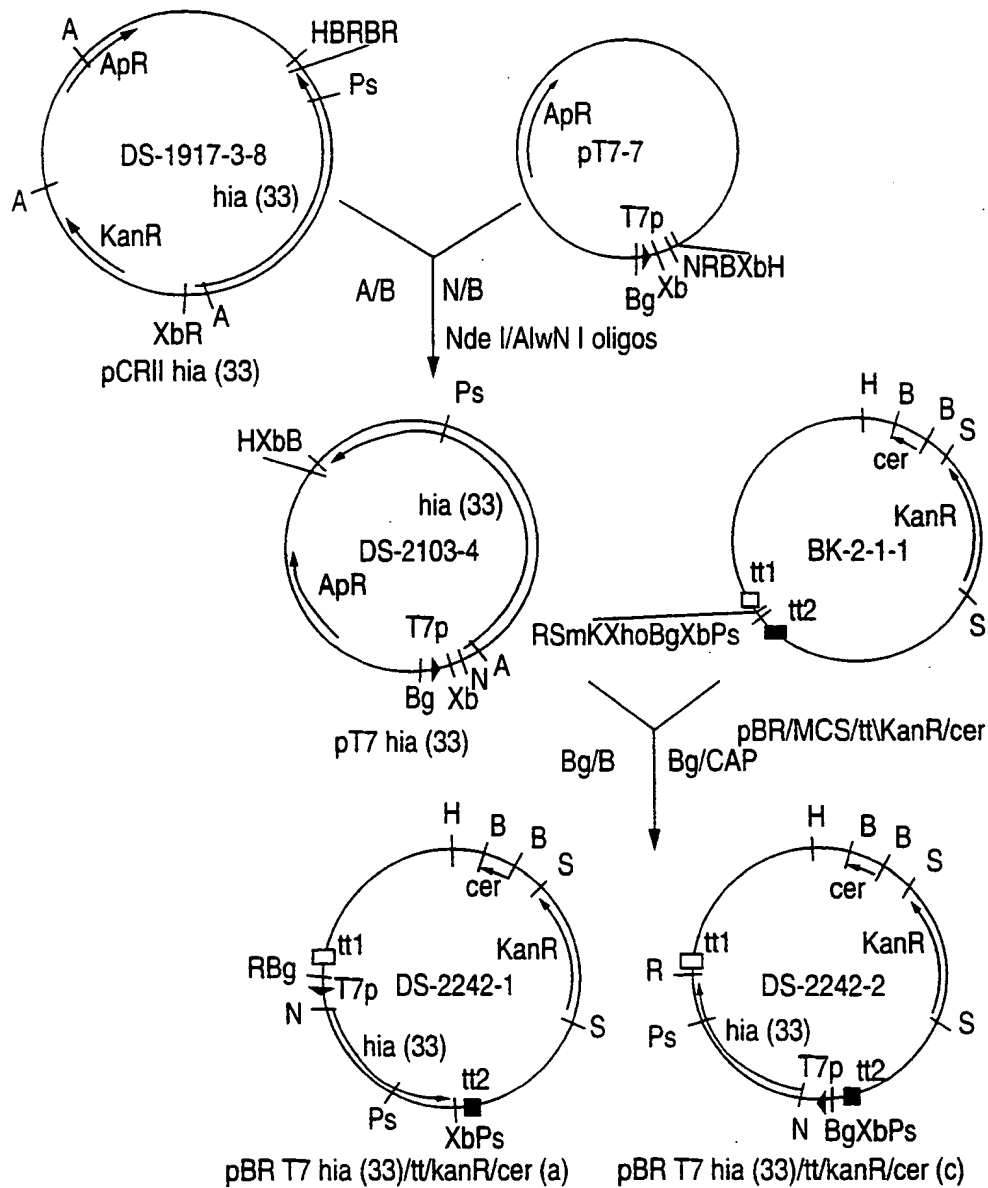


FIG.7A



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TTTTT "29999999"

FIG.7B

Oligonucleotides used to generate the 5'-end of the strain 33 hia gene for expression studies.

Nde I
↓
M N K I F N V I W N V M T Q T W A V V S E L T R A H T K...
TATGAACAAAATTTTAAACGTTATTTGGAAATGTTATGACTCAAACTTGGGCTGTCG
TATCTGAACCTACTGCGCGCCACACCA...
ACTTGTTTAAAAATTGCAATAAACCTTACAATACTGAGTTT
GAACCGACACCATAGACTTCAGTGAAGCGCGGCTGTGGT...
... R A S A T V A A SEQ ID NO:54
...AACGTGCTCCCTCCGCAACCGTGGCAGCG SEQ ID NO:52
...TTGCACGGAGCGGTTGGCACCGTC SEQ ID NO:53
...
AlwN I



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Construction of DS-2340-2-3,
a plasmid containing T7 V38 hia (33) and cer.

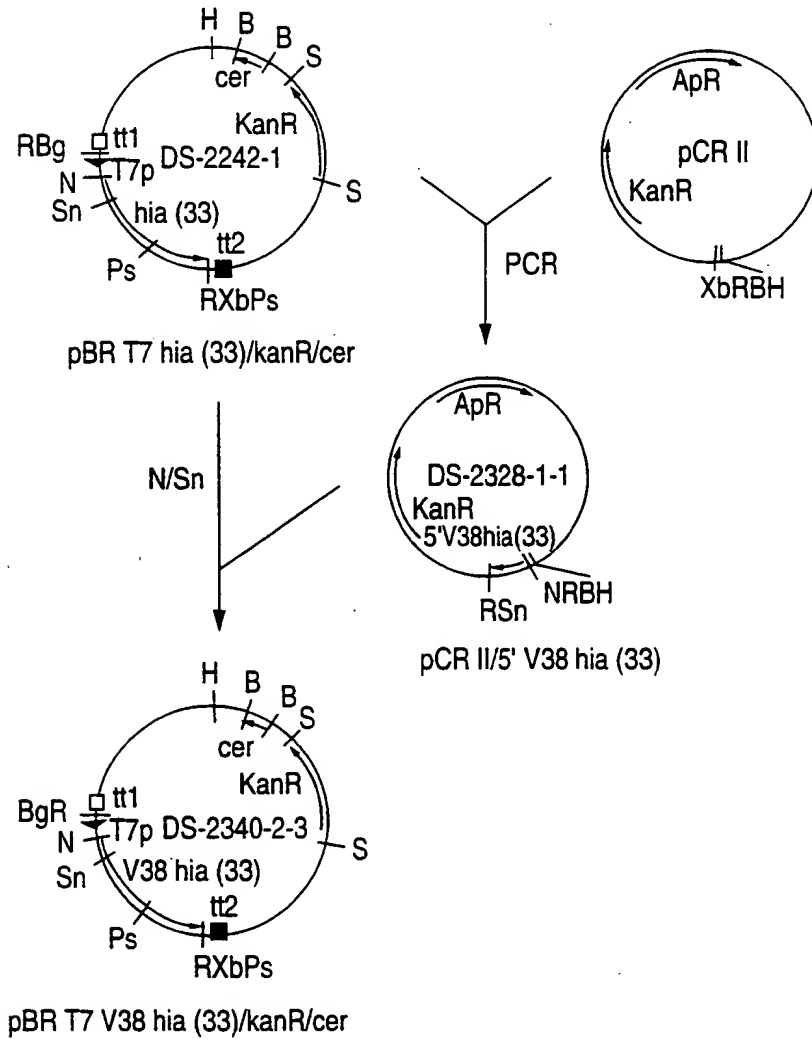


FIG.8A

[illegible]

oligonucleotides used to PCR amplify the strain 33 *hla* gene from the V38 codon to the SnaB I site.

3'

3'

5'

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Construction of DS-2447-2,
a plasmid containing tandem T7 V38 hia (11) cassettes and cer.

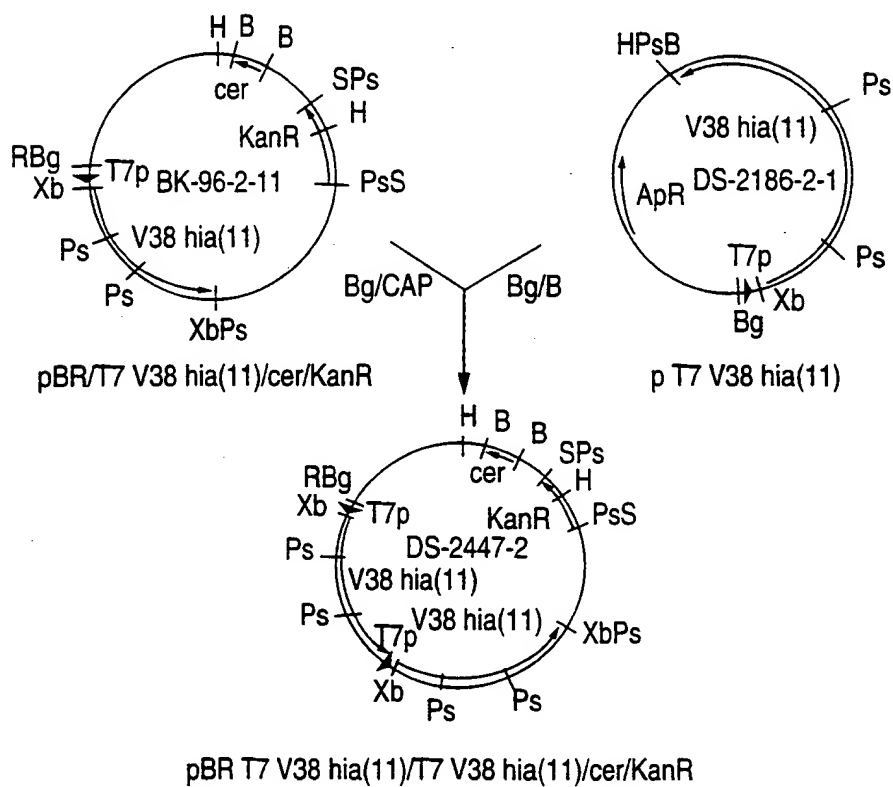


FIG.9A

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Construction of DS-2448-17,
a plasmid containing tandem T7 V38 hia(33) cassettes and cer.

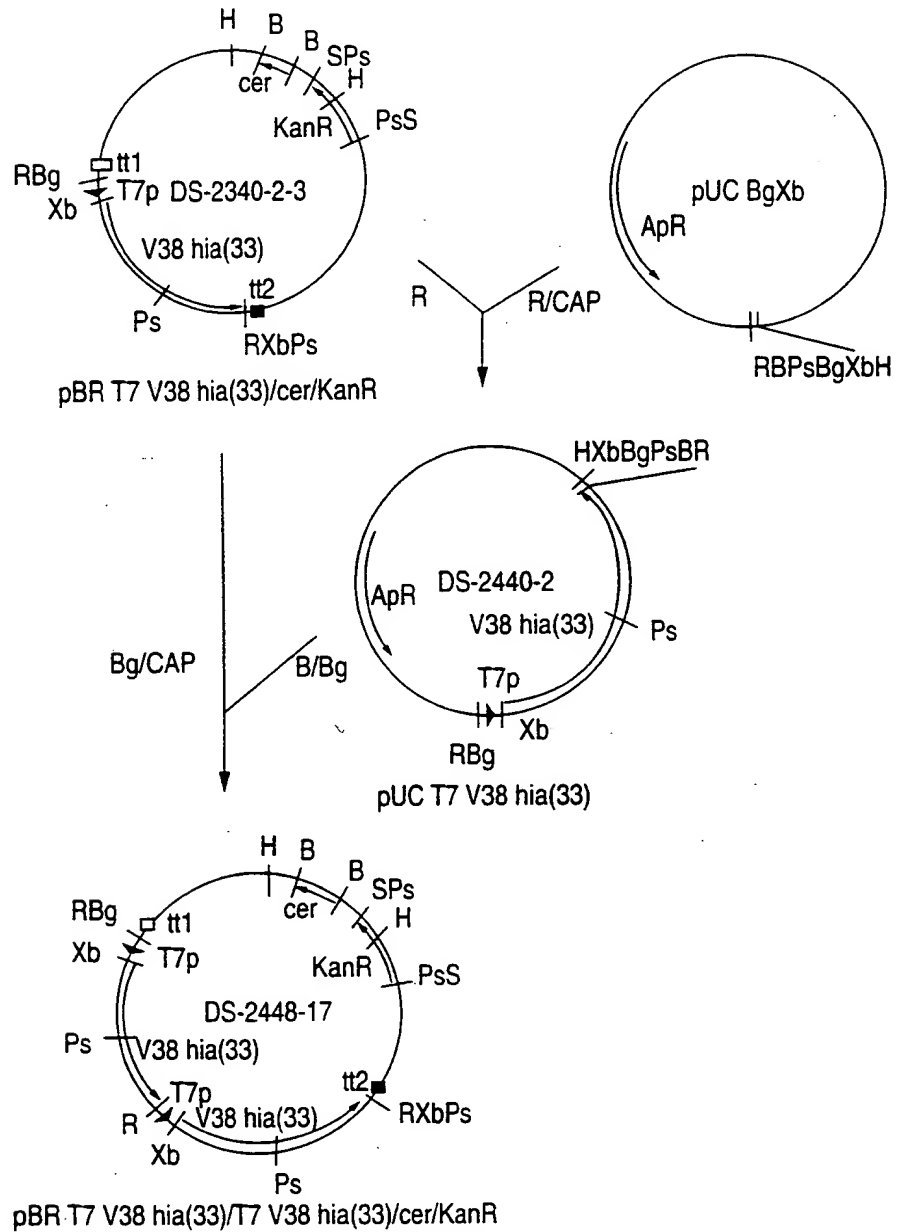
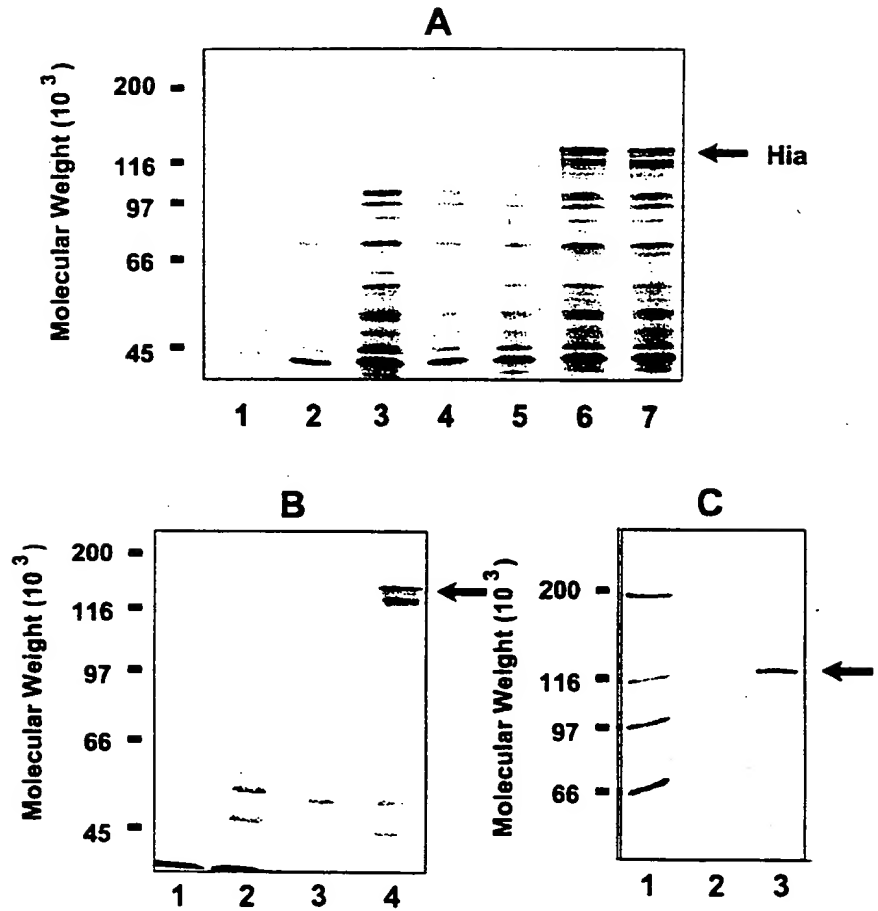


FIG.9B

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FIG.10



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Purification of rHia Proteins from E. coli

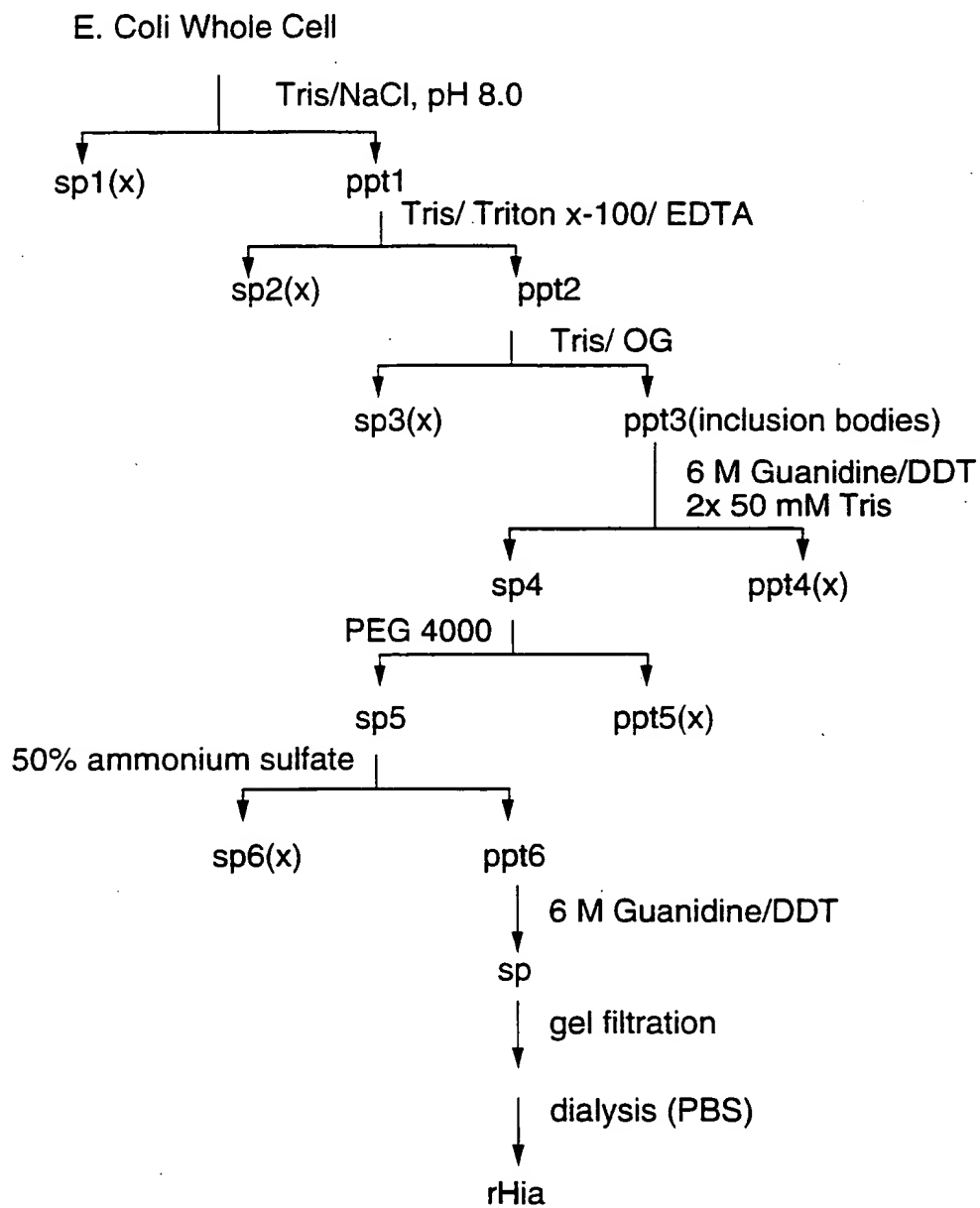
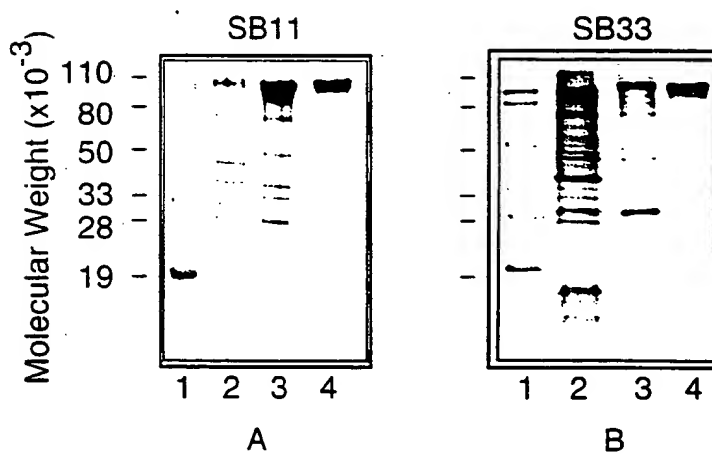


FIG.11

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Purification of rHia (V38) from E. coli



1. Prestained molecular weight markers
2. E. coli whole cell lysate
3. Crude extract
4. Purified rHia protein

FIG.12

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The Stability of rHia (V38/SB11)

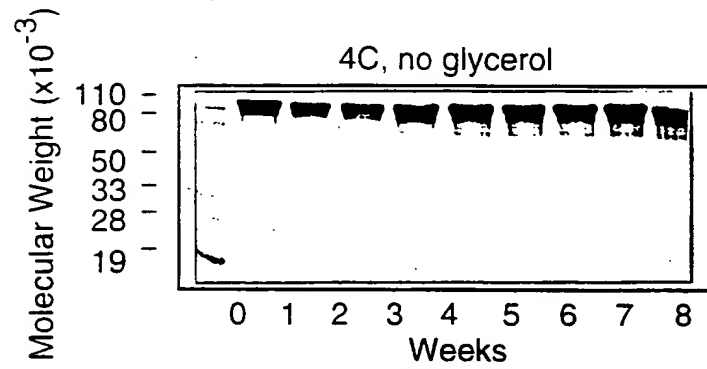


FIG.13A

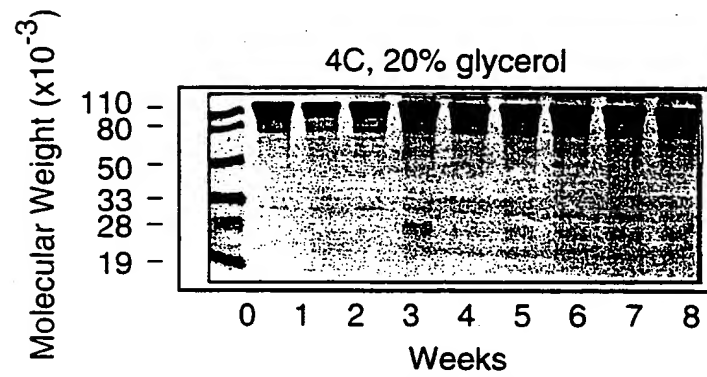


FIG.13B

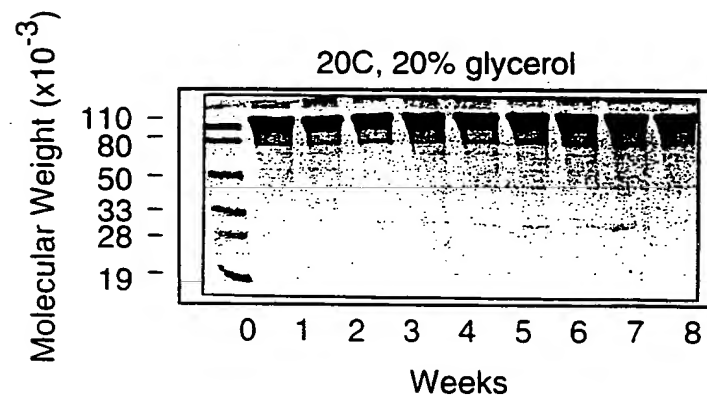


FIG.13C

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Anti-rHia (V38) Antibody Titers in Mice

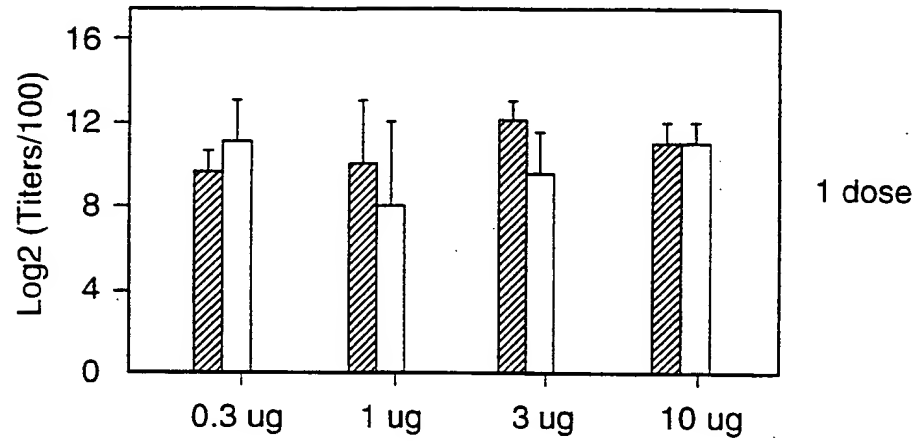
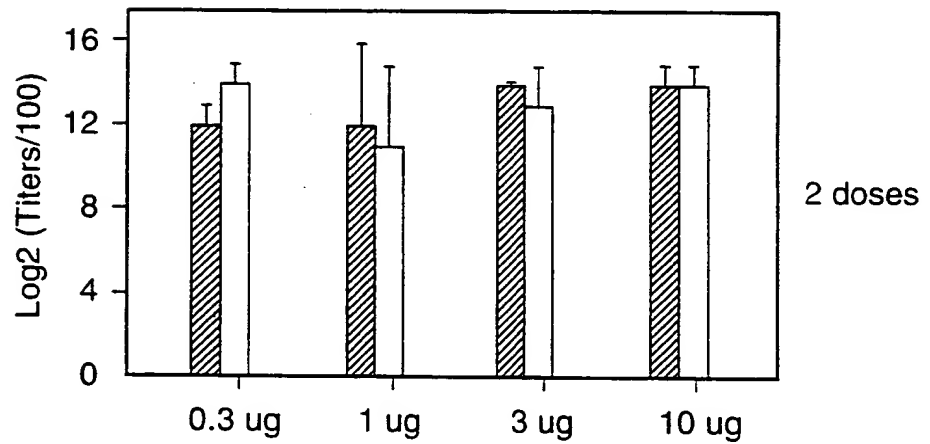


FIG.14A



SB11
SB33

FIG.14B

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Anti-V38 rHia (SB11) Antibody Titers in BALB/c Mice

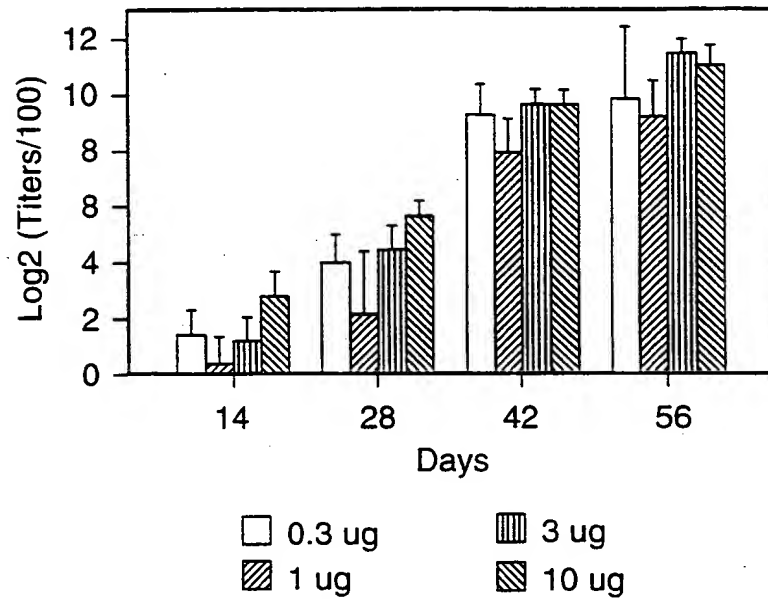


FIG.15A

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Anti-V38 rHia (SB11) Antibody Titers in Guinea Pigs

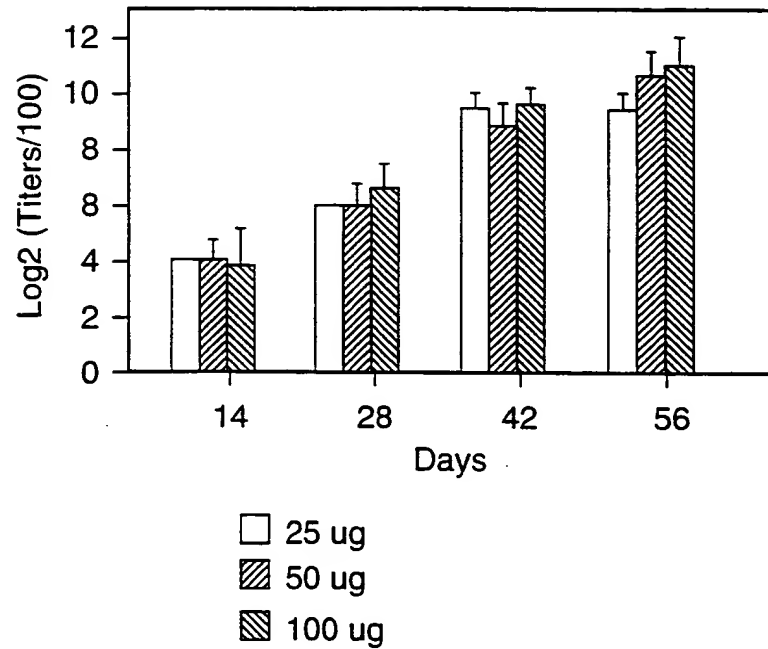


FIG.15B

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FIG. 16

Protective Ability of rHia (V38/SB33) Against
NP Colonization with NTHi Strain 33 in Chinchillas

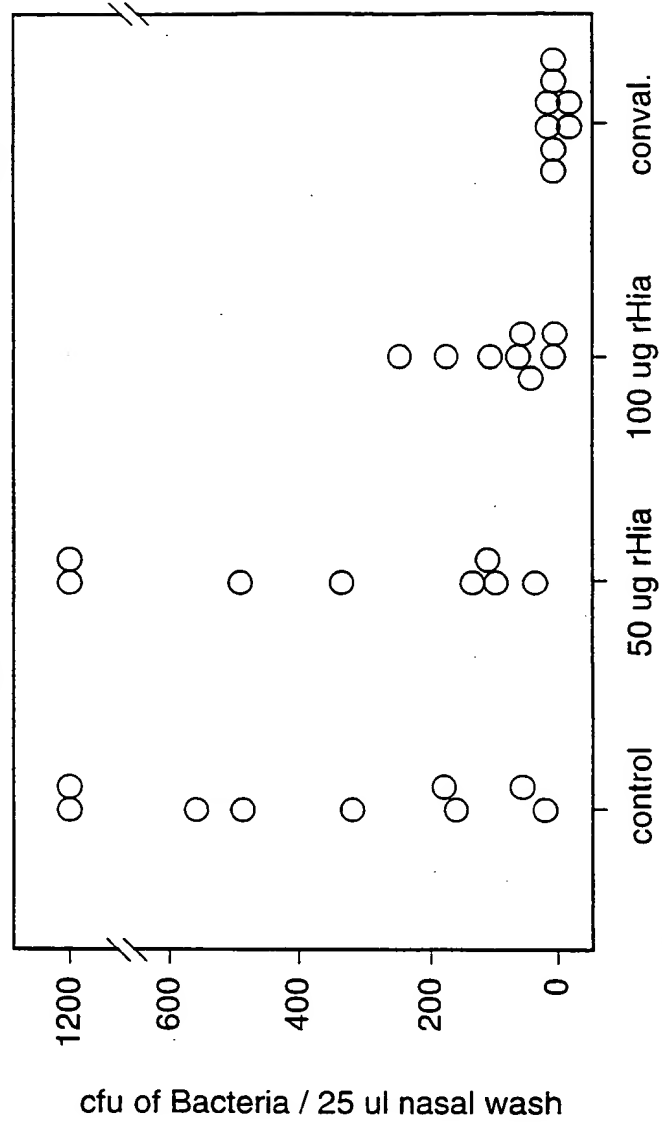


FIG.16

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FIG. 17

FIG. 17

Oligonucleotides used to PCR amplify additional *hia* genes.

sense

5' TTAATATAAGGTAAATAAAATGACAAATTTTAAAGTT 3' 5040.SL
M N K I F N V
SEQ ID NO:22
SEQ ID NO:21

antisense

5' AAAACAGCGGTTGCAGCAGGTTGGTTACCAAGTGTATAG 3'
3' TTTTGTCGCAACGTCGTCCACAAACCAATGTCACCAATTATCTTAAGCGCTAGCGG 5' 5039.SL
K T G V A A G V G Y Q W * *
↑ ↑
EcoR I BamH I

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TABLE 26-2959660

FIG.18A

NH1 strain 33 Hia

GAATTCGGCTTAAATAAAATGAACAA...	MET ASN LYS...
10	20
... ILE PHE ASN VAL ILE TRP ASN VAL MET THR GLN	
...AATTTTAAACGTTATTGGAATGTTATGACTCA	40
... 30	50
THR TRP ALA VAL VAL SER GLU LEU THR...	
70	80
AACTTGGGCTGTCGTATCTGAACCTCAC...	
... ARG ALA HIS THR LYS ARG ALA SER ALA THR VAL	
...TCGCGCCACACCAACGTCGCTCCGCAACCGT	110
... 90	120
ALA ALA ALA VAL LEU ALA THR VAL LEU...	
130	140
GGCAGCCGCTGTATTGGCGACCGTATT...	
... SER ALA THR VAL GLN ALA SER ALA GLY SER THR	
...GTC TGCAACGGTTTCAGGCGAGTGCGAGGCAGTAC	170
... 150	180
THR GLY THR ASN SER LEU ASN VAL TYR...	
190	200
GACAGGTACAAATAGTTTGAATGTTTA...	

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FIG.18B

FIG.18B 2989666

... GLY LYS ASN ASN SER ASN PHE ASN SER ALA ASN
...TGGAAAGAAATAATTCCGAATTTCATTTCAGCCAA 240
... 210 220 230

ASN SER ILE ALA ASP LEU ASN LYS GLN...
TAATTCAATAGCAGATTATAATAACA... 250
... 260
... ASN ASP SER VAL TYR ASP GLY LEU ASN LEU
...AATGATAGTGTTTACGATGGTTTATAAATCT 280 290 300
... 270

ASN GLU LYS GLY THR ASP LYS SER LYS...
GAATGAAAGGACGATAGTCAA... 310
... 320
... PHE LEU VAL ALA ASP GLU THR ALA THR VAL
...ATTCTGGTTGCTGACGAAACCAACCGCAACCGT 340 350 360
... 330

GLY ASN LEU ARG LYS LEU GLY TRP VAL...
AGGCAATTACGTAATAATTGGGTTGGGT... 370
... 380
... VAL SER THR LYS ASN SER THR LYS GLU SER
...AGTATCAACCAAAACACAGTACGAAAGAAAG 410 420
... 390 400

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FIG. 18C

FIG. 18C

ASN GLN VAL LYS GLN ALA ASP GLU VAL...
CAATCAAGTCAACACAGCGGATGAAGT...
430 440
... LEU PHE GLU GLY LYS ASP GLY VAL THR VAL THR
... GTTGTGTAAGGCAAGACGGGTGTAACGGTTAC
450 460 470 480

SER LYS SER GLU ASN GLY LYS HIS THR...
TTCCAAATCTGAACGCGGCAACACAC...
490 500
... VAL THR PHE ALA LEU ALA ASN ASP LEU ASN VAL
... CGTTACTTTTGGCCCTTGCGGAATGACCTTAATGT
510 520 530 540

LYS ASN ALA THR VAL SER ASP LYS LEU...
AAAAACGCAACCGTTAGCGATAAATT...
550 560
... SER LEU GLY ALA ASN GLY LYS VAL ASP ILE
... ATCGCTTGGTGCAACCGGCAAGAAAGTCGATAT
570 580 590 600

THR SER ASP ALA ASN GLY LEU LYS PHE...
TACCAAGTGAATGCAACGCGCTTGAAATT...
610 620

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FIG. 18D

FIG. 18D

... ALA LYS GLN GLY THR ASN GLY GIN ASN GLY ASN
...T GCG A A A C A G G G T A C G A A T G G T C A A A C G G T A A
... 630 640 650 660

VAL HIS LEU ASN GLY ILE ALA SER THR...
T G T T C A C T T A A A C G G T A T T G C T T C G A C ...
670 680
... LEU ASP ASP PRO ARG VAL GLY GLY LYS THR ALA
...T T A G A T G A T C C T C G T G T G G G T G G A A A A C A C G C
... 690 700 710 720

HIS LEU THR LYS GLU ILE SER ASP THR...
A C A C C T T A C A A A G A A A T C A G C G A T A C ...
730 740
... GLU ARG ASN ARG ALA ALA SER VAL GLY ASP VAL
...A G A C G T A A C C G T G C T G C G A G C G T G G G C G A T G T
... 750 760 770 780

LEU ASN ALA GLY TRP ASN ILE ARG GLY...
A T T G A A T G C G G G T T G G A A T A T T C G T G G ...
790 800
... ALA LYS THR ILE GLY GLY THR VAL ASP ASN VAL
...C G C A A A A C G A T T G G C G G T A C A G T G G A T A A T G T
... 810 820 830 840

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FIG. 18E

FIG. 18E

ASP PHE VAL SER THR ASP THR VAL...
TGATTTTGTTCACCTTATGACACTGT...
850
... GLU PHE ALA SER GLY ALA ASN ALA ASN VAL SER
...TGAAATTGCCAGCGCGCAACGCAAAATGTGAG
880
... 870 890 900

VAL THR THR ASP ASP ASN LYS LYS THR...
CGTTACGACTGATGATAACAATAAAC...
910
... THR VAL ARG VAL ASP VAL THR GLY LEU PRO VAL
...AACCGTCCGTGTGGATGTACAGGCTTGCCGGT
930 940 950 960

GLN TYR VAL THR GLU ASP SER LYS THR...
CCAATATGTTACGGGAAGACAGCAAAAC...
970
... VAL VAL LYS VAL GLY ASN GLU TYR GLU ALA
...CGTTGTGAAGTGGGCAATGAGTATACGAAGC
980 990 1000 1010 1020

LYS GLN ASP GLY SER ALA ASP MET ASP...
CAGCAAGACGGTTCGGCGGATATGGA...
1030 1040

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FIG.18F

FIG.18F 2959550

... LYS LYS VAL GLU ASN GLY LYS LEU ALA LYS THR
...TAA A A A G T C G A A A T G G C A A G C T G G C G A A A C
... 1050 1060 1070 1080

LYS VAL LYS LEU VAL SER ALA ASN GLY...
TAAAGTGAAATTGGTATTCGGCAACGG...
1090 1100

... THR ASN PRO VAL LYS ILE SER ASN VAL ALA ASP
...TACAAATCCGGTGAAATCAGCAATGTTGCCGA
... 1110 1120 1130 1140

GLY THR GLU ASP THR ASP ALA VAL SER...
CGGCACGGAGATACCGATGCCGGTCAG...
1150 1160

... PHE LYS GLN LEU LYS ALA LEU GLN ASP LYS GLN
...CTTAAGCAGTTGAAAGCCCTTGCAAGATAACA
... 1170 1180 1190 1200

VAL THR LEU SER ALA SER ASN ALA TYR...
GGTTACGTTAAGTGCGAGCAATGCTTA...
1210 1220

... ALA ASN GLY SER ASP ALA ASP GLY GLY LYS
...TGCCCAATGGCGGTAGCGATGCCGACGGCGGCA
... 1230 1240 1250 1260

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SEQUENCE

FIG.18G

ALA THR GLN THR LEU GLY ASN ASP LEU...
GGCAACTCAAACTTTAGGCAATGATTT...
1270
... ASN PHE LYS SER THR ASP SER GLU LEU
...GAAATTTTAAATTTAAATCCACAGACAGCGAGTT
1280
... 1290 1300 1310 1320

LEU ASN ILE LYS ALA ALA GLY ASP THR...
GTTGAACATCAAGCAGCAGGAGTGACAC...
1330
... VAL THR PHE THR PRO LYS LYS GLY SER VAL GIN
...GGTTACCTTTACGCCGAAATAAGGTTTCGGTGCA
1340
... 1350 1360 1370 1380

VAL GLY ASP ASP GLY LYS ALA THR ILE...
GGTTGGCGATGATGGTAAGGCTACGAT...
1390
... GIN ASP GLY ALA LYS THR THR THR GLY LEU VAL
...TCAAGACGGCGGAAACAACAATAACCGGTTTGGT
1400
... 1410 1420 1430 1440

GLU ALA SER GLU LEU VAL ASP SER LEU...
TGAGGCTTCTGAATTGGTTGACAGCCT...
1450
... 1460

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FIG.18H

TOGETHER 2999566

... ASN LYS LEU GLY TRP LYS VAL GLY VAL GLY LYS
...G A A C A A A T T G G C T G G A A A G T G G C G T T G G T A A
... 1470 1480 1490 1500

ASP GLY THR GLY ALA THR ASP GLY THR...
A G A C G G C A C A G G A G C C G A T G G C A C ...
1510 1520
... HIS THR ASP THR LEU VAL LYS SER GLY ASP LYS
...G C A T A C C G A C A C T T T A G T G A A G T C G G C G A T A A
... 1530 1540 1550 1560

VAL THR LEU LYS ALA GLY ASP ASN LEU...
A G T A A C T T T G A A A G C C G G C G A T A T C T ...
1570 1580
... LYS VAL LYS GLN GLU GLY THR ASN PHE THR TYR
...G A A G G T C A A C A A G A G G G T A C A A C T T C A C T T A
... 1590 1600 1610 1620

VAL LEU ARG ASP GLU LEU THR GLY VAL...
C G T G C T C A G A G A T G A A T T G A C G G C G T ...
1630 1640
... LYS SER VAL GLU PHE LYS ASP THR GLU ASN GLY
...A A A G A G C G T G G A G T T T A A G A C A C G G A G A A T G G
... 1650 1660 1670 1680

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FIG. 18I

FIG. 18I

ALA ASN GLY ALA SER THR LYS ILE THR...
TGCAACGGTGCAAGCAGCAAGATTAC...
1690
... LYS ASP GLY LEU THR ILE THR PRO ALA ASN ASP
...CAAAGACGGCTTGACCATTCAGCCGGCAACGA
1710 1720 1730 1740

ALA ASN GLY ALA ALA THR ASP ALA...
TGCGAATGGTGCGGCGGCACTGATGC...
1750
... ASP LYS ILE LYS VAL ALA SER ASP GLY ILE SER
...TGACCAAGATTAAAGTGGCTTCAGACGGCATTAG
1770 1780 1790 1800

ALA GLY ASN LYS ALA VAL LYS ASN VAL...
TGCGGGTAATAAGCAGTTAAACGTT...
1810
... VAL SER GLY LEU LYS LYS PHE GLY ASP ALA ASN
...TGAGCGGACTGAAGAAATTTGGTGATGCCGA
1830 1840 1850 1860

PHE ASN PRO LEU THR SER SER ALA ASP...
TTTCAATCCGCTGACTAGCTCAGCCGA...
1870 1880

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TTTTT"29999999

FIG.18J

... ASN LEU THR LYS GLN TYR ASP ASN ALA TYR LYS
...CAACTTAACGAAACAATATGACCAATGCCCTATAA
... 1890 1900 1910 1920

GLY LEU THR ASN LEU ASP GLU LYS SER...
AGGCTTGACCAATCTGGATGAAAAAG...
1930 1940
... LYS GLY LYS GLN THR PRO THR VAL ALA ASP ASN
...TAAGGCAAGCAAACTCCGACCGTTGCTGACAA
... 1950 1960 1970 1980

THR ALA ALA THR VAL GLY ASP LEU ARG...
TACCGCTGCAACCGTGGGCGATTGCG...
1990 2000
... GLY LEU GLY TRP VAL ILE SER ALA ASP LYS THR
...CGGTTTGGGCTGGGTCAATTTCTGCAGACAAAC
... 2010 2020 2030 2040

THR GLY GLU SER LYS GLU TYR SER ALA...
CACAGGCGAGTCAAGGAATATAGCGC...
2050 2060
... GLN VAL ARG ASN ALA ASN GLU VAL LYS PHE LYS
...GCAAGTGCGTAACGCCCAATGAAGTGAATTCAA
... 2070 2080 2090 2100

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FIG. 18K

FIG. 18K

SER GLY ASN GLY ILE ASN VAL SER GLY...
GAGCGGCAACGGTATCAATGTTTCCGG...
2110
... LYS THR LEU ASP ASN GLY THR ARG GLU ILE THR
...TAAACAATTGGATAACGGTACGGCGGAATATC
... 2130 2140 2150 2160

PHE GLU LEU ALA LYS ASP GLU ASN ALA...
TTTGAATTGGCTAAAGACGAAATGC...
2170
... ILE ALA PHE GLY SER LYS ALA LEU ARG
...CATTGCTTTCGGTTCTGGCTCAAAAGCCCTTGCG
... 2190 2200 2210 2220

ASP ASN THR VAL ALA ILE GLY THR GLY...
CGATAACACGGTGGCGATTGGTACGGG...
2230
... ASN VAL VAL ASN ALA GLU LYS SER GLY ALA PHE
...CAACGTTGTGAATGCGGAAATACTGGTGCAATT
... 2250 2260 2270 2280

GLY ASP PRO ASN TYR ILE GLU ASP LYS...
CGCGGATCCGAACCTACATCGAAGATAA...
2290 2300

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FIG.18L

TTTATT TTTTGGG

... ALA GLY GLY SER TYR ALA PHE GLY ASN ASP ASN
...AGCCGGTGGCAGCTACGCTTTCGGTAACGATAA 2340
... 2310 2320 2330

ARG ILE THR SER LYS ASN THR PHE VAL...
CCGTATTACTTCTTAAACACTTTTGT... 2350
... LEU GLY ASN GLY VAL ASN ALA LYS TYR LYS ALA
...GTTGGGTAATGGAGTTAATGCCGAATAATAAGC 2400
... 2370 2380 2390

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ASN GLY ASP VAL ASP THR GLU THR VAL...
CAATGGAGATGTTGATACCGAATACCGT... 2410
... THR VAL LYS ASP LYS ASP GLY LYS GLU THR THR
...AATGTTTAAAGGACAAAGACGGTAAGAGACTAC 2460
... 2430 2440 2450

VAL THR VAL PRO LYS ALA LEU GLY ALA...
CGTTACTGTTCCCTAAAGCGTTAGGGGC... 2470
... THR VAL GLU ASN SER VAL TYR LEU GLY ASN LYS
...TACGGTTGAAACTCCGTTTATTGGGTAATAA 2520
... 2490 2500 2510

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FIG.18M

SER THR ALA THR LYS ASP LYS GLY LYS...
ATCGACTGCGGACAAAGATAAGGGTAA...
2530
... ASN LEU LYS SER ASP GLY THR ALA GLY ASN THR
...AATCTGAATCTGATGGTACGGCGGGTAAACAC
2540
... 2550 2560 2570 2580

THR THR ALA GLY THR THR GLY THR VAL...
TACAACTGCTGGTACACAGGGGTACGGT...
2590
... ASN GLY PHE ALA GLY ALA THR ALA HIS GLY ALA
...AACGGCTTTGCCGGTGCAACGGCGCACGGGTGC
2600
... 2610 2620 2630 2640

VAL SER VAL GLY ALA SER GLY GLU...
GGTTCTCTGCGCGCAAGCGCGGAAGA...
2650
... ARG ARG ILE GLN ASN VAL ALA GLY GLU ILE
...AGACGTATCCAAACGTGCGGCAGCGGAAT
2660
... 2670 2680 2690 2700

SER ALA THR SER THR ASP ALA ILE ASN...
TCCGGCTACTTCCACCGATGCGATTAA...
2710
... 2720

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FIG.18N

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... GLY SER GIN LEU TYR ALA VAL ALA LYS GLY VAL
...CGGCAGCCAGTTGTATGCCCGTGGCAAAAGGGGT 2760
... 2730 2740 2750

THR ASN LEU ALA GLY GIN VAL ASN LYS...
AACAAACCTTGCTGGACCAAGTGAAATAA... 2770
... 2780

... VAL GLY LYS ARG ALA ASP ALA GLY THR ALA SER
...AGTGGGCAAAACGTGCAGATGCAGGTACAGCAAG 2820
... 2790 2800 2810

ALA LEU ALA ALA SER GIN LEU PRO GIN...
TGCAATTAGCGGCTTCAACAGTTACCACA... 2830
... 2840

... ALA SER MET SER GLY LYS SER MET VAL SER ILE
...AGCCTCTATGTCAGGTAAATCAATGTTTCTAT 2880
... 2850 2860 2870

ALA GLY SER SER TYR GIN GLY GIN SER...
TCCGGGAAGTAGTTATCAAGGTCAAAG... 2890
... 2900

... GLY LEU ALA ILE GLY VAL SER ARG ILE SER ASP
...TGGTTTAGCTATCAGGGGTATCAAGAAATTTCCGA 2940
... 2910 2920 2930

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FIG. 180

FIG.180

```
ASN GLY LYS VAL ILE ARG LEU SER...  
T A A T G G C A A A G T G A T T A T T C G C T T G T C ...  
2950  
...  
... GLY THR THR ASN SER GLN GLY LYS THR GLY VAL  
...A G G C A C A C C C A A T A G C C A A G G T A A A C A G G C G T 3000  
... 2970 2980 2990  
ALA ALA GLY VAL GLY TYR GLN TRP ***  
T G C A G C A G G T G T T G G T T A C C A G T G G T A ...  
3010 3020 ...  
...A T A G A A T T C  
... 3030
```

FIG. 19A

FIG. 19A

NH1 strain 32 hia

GAATTCCGGCCTTTAAATATAAGGTAATAA... 20 30 ...

...AATGAACAAATTTTAAACGTTATTGGAA 40 50 60

... MET ASN LYS ILE PHE ASN VAL ILE TRP ASN

... TGTGTGACTCAAACTTGGGTTGTCGTATC... 70 80 ...

... GLU LEU THR ARG THR HIS THR LYS CYS ALA 90 100 110 120

... TGAACCTCACTCGCACCCACCAAAATGCGC 100 110 120

VAL VAL THR GLN THR TRP VAL VAL VAL SER... 70 80 ...

CTCCGCCACCGTGCGCAGTTGCCGTTATGGC... 130 140 ...

... THR LEU LEU SER ALA THR VAL GLN ALA ASN 150 160 170 180

... AACCCCTGTTGTCGCAACGGTTCAGCGCAA 160 170 180

... ALA THR ASP GLU ASN GLU ASP GLU GLU... 190 200 ...

TGCTACCGATGAACGAAAGATGATGAAGA... 190 200 ...

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[illegible]

FIG. 19B

... GLU LEU GLU PRO VAL GLN ARG SER VAL LEU
A G A G T T A G A A C C C G T A C A A C G C T C T G T T T
 220 230 240

ARG TRP SER PHE LYS SER ALA LYS GLU GLY...
A A G G T G G A G C T T C A A T C C G C T A G G A G G ...
250 260 270 ...

260 THR GLY GLU GLN GLU GLY THR THR VAL
...
...C A C T G G A G A C A C A G G G A C A C A G G T
 280 290 300

ILE ASN LEU ASN THR ASP SER SER GLY ASN...
AAATAATTGAAACACAGATTCTCAGGAAA...
310 320 330 ...

320 330 ... 340 350 360

... ALA VAL GLY SER SER THR ILE THR PHE LYS

...TGCAGTAGGAGAGCAGCACATCACCTTCAAC 360

ALA GLY ASP ASN LEU LYS ILE LYS GLN SER...
AGCCGGCGACAACTGAAAATCAACAAG...
370 380 390 ...

380 GLY ASN ASP PHE THR TVR SER LEU LYS
...
...C G G C A A T G A C T T C A C C T A C T C G C T G A A A
 400 410 420

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FIG.19C

GLU LEU LYS ASN LEU THR SER VAL GLU THR...
AGAGCTGA AAAACCTGACCA GTGTGAAAC...
430 440 450 ...
... GLU LYS LEU SER PHE GLY ALA ASN GLY ASN
...TGAA A A A T T A T C G T T T G G C G C A A A C G G C A A
460 470 480

LYS VAL ASP ILE THR SER ASP ALA ASN GLY...
TAAAGTTGATAT TACCA GTGATGCA AATGG...
490 500 510 ...
... LEU LYS LEU ALA LYS THR GLY ASN GLY ASN
...CTTGAA A A T T G G C G A A A C A G G T A A C G G A A A
520 530 540

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GLY GLN ASN SER ASN VAL HIS LEU ASN GLY...
TGGTC AAAACAGTAATGTTCACTTAAACGG...
550 560 570 ...
... ILE ALA SER THR LEU THR ASP THR LEU ALA
...TATGCTTCGACTTTGACCCGATACGCTTGC
580 590 600

GLY GLY THR THR GLY HIS VAL ASP THR ASN...
CGGTGGCACAACAGGACACGTTTGACACCAA...
610 620 630 ...

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FIG. 19D

FIG. 19D

... ILE ASP ALA VAL ASN TYR HIS ARG ALA ALA
...CATTGATGCGGTTAATTATCATCGCGCTGC
... 640 650 660

SER VAL GIN ASP VAL LEU ASN SER GLY TRP...
AAGCGTACAAGATGTGTTAAACAGCGGTTG...
670 680 690 ...
... ASN ILE GIN GLY ASN GLY ASN ASN VAL ASP
...GAATATCCAAAGGCAATGGAAACAATGTCTGA
... 700 710 720

PHE VAL ARG THR TYR ASP THR VAL ASP PHE...
TTTGTCCGTACTTACGACACCGTGGAATT...
730 740 750 ...
... VAL ASN GLY ALA ASN ALA ASN VAL SER VAL
...TGTC AATGGCGCGCAATGCCCAATGTGAGCGT
... 760 770 780

THR ALA ASP THR ALA HIS LYS THR THR...
TACGGCTGATACGGCTCACAAAGACAC...
790 800 810 ...
... VAL ARG VAL ASP VAL THR GLY LEU PRO VAL
...TGTCCTGTGGATGTACAGGCTTGCCGGT
... 820 830 840

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FIG.19E

GLN TYR VAL THR GLU ASP GLY LYS THR VAL...
TCAATATGTTACGGAAGACGGCAAAACCGT...
850 ... VAL LYS VAL GLY ASN GLU TYR LYS ALA
...TGTGAAAGTGGGCAATGAGTATTACAAAGC
880 ... 890 900

LYS ASP ASP GLY SER ALA ASP MET ASN GLN...
CAAGATGACGGTTTCGGCGGATATGAATCA...
910 ... LYS VAL GLU ASN GLY LEU ALA LYS THR
...AAGTCGAAACCGCGAGCTGGCGAAAC
940 ... 950 960

LYS VAL LYS LEU VAL SER ALA SER GLY THR...
CAAGTGAAATTGGGTATCGGCAAGCGGTAC...
970 ... ASN PRO VAL LYS ILE SER ASN VAL ALA ASP
...AATCCGGTGAAATTAGCAATGTTGCAGA
1000 ... 1010 1020

GLY THR GLU ASP THR ASP ALA VAL SER PHE...
CGGCACGGGAAGACACCGGATGCGGTCAAGCTT...
1030 ... 1040 1050 ...

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FIG.19F

FIG.19F 2999660

... LYS GIN LEU LYS ALA LEU GIN ASP LYS GIN
...TAA GCAATTAAAGCCCTTGCAAGACAAACA 1080
... 1060 1070 1080

VAL THR LEU SER THR SER ASN ALA TYR ALA...
GGTTACGTTGAGCAGCAATGCTTATGC... 1090
... 1100 1110 ...

... ASN GLY THR ASP ASN ASP GLY LYS
...CAATGGCGGTACAGATAACGACGGCGGCAA 1140
... 1120 1130 1140

ALA THR GIN THR LEU SER ASN GLY LEU ASN...
GGCAACTCAACTTTAAGCAATGGTTTGAA... 1150
... 1160 1170 ...

... PHE LYS PHE LYS SER SER ASP GLY GLU LEU
...TTTAAATTATAATCTAGCGATGGCGAGTT 1200
... 1180 1190 1200

LEU LYS ILE SER ALA THR GLY ASP THR VAL...
GTTGAAATAATAGCGCGGACCGGCGATACGGT... 1210
... 1230 ...

... THR PHE THR PRO LYS LYS GLY SER VAL GIN
...TACTTTTACGCCGAAATAAGGTTCCGGTACA 1260
... 1240 1250 1260

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TTTCTT' ASP GGGG

FIG.19G

VAL GLY ASP ASP GLY LYS ALA SER ILE SER...
GGTTGGCGGATGATGGCAAGGCTTCAATTTC...
1270 1280 1290 ...
... LYS GLY ALA ASN THR THR GLU GLY LEU VAL
...AAGGTGCAATAACAACCTGAAGGTTTGGT
1300 1310 1320

GLU ALA SER SER GLU LEU VAL GLU SER LEU ASN...
TGAGGCTTCTGAATTGGTTGAAAGCCTGAA...
1330 1340 1350 ...
... LYS LEU GLY TRP LYS VAL GLY VAL GLU LYS
...CAACCTGGGTGGAAAGTAGGGGTTGAGAA
1360 1370 1380

VAL GLY SER SER GLY GLU LEU ASP GLY THR SER...
AGTCGGCAGCGCGGAGCTTGATGGTACATC...
1390 1400 1410 ...
... LYS GLU THR LEU VAL LYS SER GLY ASP LYS
...CAGGAAACTTTAGTGAAAGTCGGGCGGATAA
1420 1430 1440

VAL THR LEU LYS ALA GLY ASP ASN LEU LYS...
AGTAACCTTTGAAAGCCGGCGCAATCTGAA...
1450 1460 1470 ...

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FIG. 19H

FIG. 19H

... VAL LYS GLN GLU GLY THR ASN PHE THR TYR
...GGTCAAACAAGAGGGCACAAACTTCACTTA 1500
... 1480 1490

ALA LEU LYS ASP GLU LEU THR GLY VAL LYS...
CGCGCTCAAGAATGACGGGCGTGAA... 1530 ...
... SER VAL GLU PHE LYS ASP THR ALA ASN GLY
...GAGCGTGGAGTTTAAAGACACGGCGAATGG 1560
... 1540 1550

ALA ASN GLY ALA SER THR LYS ILE THR LYS...
TGCAACCGGTGCAAGCACGAAGATTACCA... 1590 ...
... ASP GLY LEU THR ILE THR LEU ALA ASN GLY
...AGACGGCTTGACCATTAACGCTGGCAACGG 1620
... 1600 1610

ALA ASN GLY ALA THR VAL THR ASP ALA ASP...
TGCGAATGGTGCGGACGGTGACTGATGCCGA... 1650 ...
... LYS ILE LYS VAL ALA SER ASP GLY ILE SER
...CAAGATTAAAGTTGCTTCGGACGGCATTAG 1680
... 1660 1670

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FIG. 191

FIG.191

ALA GLY ASN LYS ALA VAL LYS ASN VAL ALA...
CGCGGGTAATAAGCAGTTAAACGTCGC...
1690 1700 1710 ...
... ALA GLY GLU ILE SER ALA THR SER THR ASP
...GGCAGGCGAAATTTCTGCCACTTCCACCGA
1720 1730 1740

ALA ILE ASN GLY SER GIN LEU TYR ALA VAL...
TGCGATTACGGGAAGCCAGTTGTATGCCGT...
1750 1760 1770 ...
... ALA LYS GLY VAL THR ASN LEU ALA GLY GIN
...GCCAAGGGGTAAACAACCTTGCTGGACA
1780 1790 1800

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VAL ASN ASN LEU GLY LYS VAL ASN LYS...
AGTGAATAATCTTGAGGGCAAGTGAAATAA...
1810 1820 1830 ...
... VAL GLY LYS ARG ALA ASP ALA GLY THR ALA
...AGTGGGCAACGTGCAGATGCAGGTACTGC
1840 1850 1860

SER ALA LEU ALA ALA SER GIN LEU PRO GIN...
AGTGCAATAGCGGCTTCACAGTTACCAACA...
1870 1880 1890 ...

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[illegible][illegible]

ILE	ALA	GLY	SER	SER	TYR	GLN	GLY	GLN	ASN...
TAT	GCG	GGA	AGT	AGT	TAT	CAG	GTC	A A A	...
									1930
									1940
									1950 ...
									1960

ASP ASN GLY LYS VAL ILE ILE ARG LEU SER...
CGATAATGGCAAGTGAATTATTCGCTTGTC...
2000 2010 ...
... GLY THR ASN
...AGGCAACCAAT
2020

VAL ALA ALA GLY VAL GLY TYR GLN TRP ***
CGT G C A G C A G G T G T T G G T A C C A G T G G T A ...
...A T A G A A T T C

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FIG.20A

NIHi strain 29 Hia

TTGCTT-29999999

TTAAATATAAGGTAAATAAATAAGAACAA...
10 20 30...
... ILE PHE ASN VAL ILE TRP ASN VAL VAL THR
... ATTTTAAACGTTATTGGAATGTTGTGACT
40 50 60

GLN THR TRP VAL VAL VAL SER GLU LEU THR ...
CAAACTTGGGTTGTCGTATCTGAACCTCACT...
70 80 90...
... ARG ALA HIS THR LYS CYS ALA SER ALA THR
... CGCGCCCAACCAAAATGCGCCTCCGCCACC
100 110 120

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VAL ALA VAL ALA VAL LEU ALA THR ALA LEU ...
GTGGCGGTTGCGCGTATTGGCAACTGCGTTG...
130 140 150...
... SER ALA THR ALA GLU ALA ASN ASN THR
... TCTGCAACGGCTGAAGCGGAACAATACT
160 170 180

SER VAL THR ASN GLY LEU ASN ALA TYR GLY ...
TCTGTACGAATGGGTTGAATGCTTATGGC...
190 200 210...

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FIG.20B

1151011 25446611

... ASP THR ASN PHE ASN THR THR ASN ASN SER
... GATACATAATTATAATACCAATAATTCCG 240
... 220 230

ILE ALA ASP LEU GLY LYS HIS VAL GIN ASP ...
ATAGCAGATTGTGAAACACGTTCAAGAT... 260
... 250 270...
... ALA TYR LYS GLY LEU LEU ASN LEU ASN GLU
... GCTTATAAAGGCTTATTAAATCTGAATGAA 300
... 280 290

LYS ASP THR ASN LYS SER PHE LEU VAL ...
AAGATACAAATAAGTCAAGTTTCTTGTT... 310
... 320 330...
... ALA ASP ASN THR ALA ALA THR VAL GLY ASN
... GCCGACAATACCGCCGCAACCGTAGGCAAT 360
... 340 350

LEU ARG LYS LEU GLY TRP VAL LEU SER ...
TTGCGTAATAATTGGGCTGGGTATTGTCTAGC... 370
... 380 390...
... LYS ASN GLY THR ARG ASN GLU LYS SER TYR
... AAAACGGCACAAAGGAACGAGAAAGCTAT 420
... 400 410

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FIG. 20C

FIG. 20C

GLN VAL LYS LYS GLN ALA ASP GLU VAL LEU PHE ...
C A G T A A A C A A G C T G A T G A A G T T C T C T T ...
430 440 450...

... THR GLY SER GLY ALA ALA THR VAL SER SER
... A C T G G A T C T G G T G C T G C A A C G G T T A G T T C C
460 470 480

SER SER LYS LYS ASP GLY LYS HIS THR ILE THR ...
A G C T C T A A A G A C G G T A A C A T A C C A T T A C C ...
490 500 510...

... ILE SER VAL THR LYS GLY SER PHE ALA GLU
... A T T T C T G T T A C C A A A G G T A G T T T G C T G A G
520 530 540

VAL LYS THR ASP ALA THR GLY GLN ...
G T A A A A C T G A T G C A A C T A C T G G A G G T C A A ...
550 560 570...

... VAL ASN ALA ASP ARG GLY LYS VAL LYS ALA
... G T A A A C G C C G A C C G T G G T A A A G T G A A A G C T
580 590 600

GLU ASP GLU ASN GLY ALA ASP VAL ASP LYS ...
G A G G A C G A G A A T G G A G C T G A T G T T G A T A A G ...
610 620 630...

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FIG. 20D

FIG. 20D

... LYS VAL ALA THR VAL LYS ASP VAL ALA LYS
... AAGTTGCCAACTGTAAAGATGTTGCTAAG 660
... 640 650

ALA ILE ASN ASP ALA ALA THR PHE VAL LYS ...
GCGATTAAACGATGCCCGCAACTTTCGTGAA... 670
... VAL GLU SER THR ASP ASP ILE GLU ASN
... GTGGAAAGCACAGATGATGACATTGAAAT 720
... 690... 710

GLY ALA ALA GLY LYS ASN GLU THR ASP ...
GGTGCTGCAGGCAAAATGAACTACAGAC... 730
... GLN ALA LEU LYS ALA GLY ASP THR LEU THR
... CAAGCTCTCAAGCAGCGGACACCTTAACC 780
... 740 750... 760 770

LEU LYS ALA GLY LYS ASN LEU LYS ALA LYS ...
TTAAAGCGGGTAAACCTTAAGCTAAG... 790
... LEU ASP GLN ASN GLY LYS SER VAL THR PHE
... TTAGACCAAAATGGTAAATCAGTAACCTTT 840
... 800 810... 820 830 840

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FIG.20E

ALA LEU ALA LYS ASP LEU ASP VAL THR SER ...
GCTTAGCGGAAAGACCTTGATGTGACCTCT...
850 860 870...
... ALA LYS VAL SER ASP LYS LEU SER ILE GLY
... CCGAAAGTGAGTGATAAGTTGTCTATTGGT
880 900

LYS ASP THR ASN LYS VAL ASP ILE THR SER ...
AAGATACGGAATAAAGTTGATATTACCACT...
910 920 930...
... ASP ALA ASN GLY LEU LYS LEU ALA LYS THR
... GATGCAAAATGGCTTGAAATTGGCGAAACA
940 950 960

GLY ASN GLY ASN GLY GLN ASN GLY ASN VAL ...
GGTAACGGAAATGGTCAAAACGGTAATGTC...
970 980 990...
... HIS LEU ASN GLY ILE ALA SER THR LEU THR
... CACTTAAATGGTATTGCTTCGACTTTGACC
1000 1010 1020

ASP THR ILE THR GLY MET THR GLN ALA ...
GATACCATTTACAGGTATGACACACACAGCA...
1030 1040 1050...

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FIG.20F

TTTTTTT*2959566A

... SER ASN GLY VAL ALA VAL GIN ASN HIS ASN 1080
... AGCAATGGCGTGGCTGTGCAGAAATCATAT 1070
... 1060

ARG ALA ALA SER VAL ALA ASP VAL LEU ASN ...
CGTGCTGCGAGTGTGGCTGATGTATAAT... 1100
... ALA GLY TRP ASN ILE GIN GLY ASN GLY ALA 1110...
... GCAGGCTGGAAATATTCAAGGCCAACGGAGCG 1130
... 1120 1140

SER VAL ASP PHE VAL ASN ALA TYR ASP THR ...
AGCGTTGATTTTGTCAAATGCTTACGACACA... 1160
... VAL ASP PHE VAL ASN GLY THR ASN THR ASN 1170...
... GTAGATTTTGTCAAATGGTACAAACACCAAT 1190
... 1180 1200

VAL ASN VAL THR THR ASP THR ALA HIS LYS ...
GTGAACGTTACGACTGTGATACGGCTCACA... 1210
... LYS THR THR VAL ARG VAL ASP VAL THR GLY 1230...
... AAGACAACCGTCCGTGTGGATGTACAGGC 1250
... 1240 1260

FIG. 20G

FIG. 20G

LEU PRO VAL GLN TYR VAL THR GLU ASP GLY ...
TTGCCGGTTTCAATATGTTACGGGAAGACGGC...
1270 1290...
... LYS THR VAL VAL LYS VAL ASP ASN LYS TYR
... AAAACCGTTGTGAAGTGGACAAATAAGTAT
1300 1310 1320

TYR GLU ALA LYS GLN ASP GLY SER ALA ASP ...
TACGAAGCTAAGCAAGACGGTTTCGGCGGAT...
1330 1350...
... MET ASP LYS LYS VAL GLU ASN GLY LEU
... ATGGATAAATAAGTCGAATAATGGCGAGCTG
1360 1370 1380

ALA LYS THR LYS VAL LYS LEU VAL SER ALA ...
GCGAAACCAAGTGAAATTGGTGTCTGGCA...
1390 1410...
... SER GLY GLN ASN PRO VAL LYS ILE SER ASN
... AGCGGTCAAAATCCGGTGAAATCAGCAAT
1420 1430 1440

VAL ALA GLU GLY THR GLU GLU ASN ASP ALA ...
GTTGCGGAAGGCAAGGGAAGAAACGATGCG...
1450 1470...

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FIG. 20H

FIG. 20H

... VAL SER PHE LYS GLN LEU LYS ALA LEU GLN 1500
... GTCAGCTTTAAGCAATTGAAAGCCTTGCAA 1490
... 1480

GLU LYS GLN VAL THR LEU THR ALA SER ASN ...
GAGAAACAGGTTACTTTAACTGCGAGCAAT... 1510
... 1520

... ALA TYR ALA ASN GLY GLY ASN ASP ALA ASP 1560
... GCTTATGCCCAATGGTGGTTAACGATGCCGAC 1550
... 1540

GLY GLY LYS ALA THR GLN THR LEU ASN ASN ...
GGCGCAAGGCAACTCAAACTTTAAACAAT... 1570
... 1580

... GLY LEU ASN PHE LYS PHE LYS SER THR ASP 1620
... GGTTTGAAATTTTAAATTTAAATCCACAGAC 1610
... 1600

GLY GLU LEU LEU ASN ILE LYS VAL GLU ASN ...
GGCGAGTTGTTGAACATCAAGTAGAAAT... 1630
... 1640

... ASP THR VAL THR PHE THR PRO LYS LYS GLY 1680
... GACACAGTTACCTTTACGCCGGAATAAAGGT 1670
... 1660

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TTTTAT" 29E9E660

FIG.20I

SER VAL GLN VAL GLY GLU ASP GLY LYS ALA ...
TCGGTACAGGTTGGCGAAGACGGTAAGGCT...
1690 1700 1710...
... THR ILE GLN ASN GLY THR LYS THR ASP
... ACGATTCAAAATGGGTACGAAACCAACCGAC
1720 1730 1740
...

GLY LEU VAL GLU ALA SER GLU LEU VAL GLU ...
GGTTTGGTTGAAGCTTCCGAAATTGGTTGA...
1750 1760 1770...
... SER LEU ASN LYS LEU GLY TRP LYS VAL GLY
... AGCCTGAACAACCTGGGCTGGAAAGTGGGC
1780 1790 1800
...

VAL ASP LYS ASP GLY SER GLY GLU LEU ASP ...
GTTGATAAAGACGGCAGCGCGAGCTTGAT...
1810 1820 1830...
... GLY ALA SER ASN GLU THR LEU VAL LYS SER
... GGTGCATCCAAATGAACCTTTAGTGAGTCCG
1840 1850 1860
...

GLY ASP LYS VAL THR LEU LYS ALA GLY GLU ...
GGCGATAAAGTAACCTTTGAAGCCGGCGAG...
1870 1880 1890...
...

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FIG.20J

TTCTCTT 22222222

... ASN LEU LYS VAL LYS GIN ASP GLY THR ASN
... AATCTGAAGGTCAACAACAGACGGCACAAAC
... 1900 1910 1920

PHE THR TYR ALA LEU LYS ASP GLU LEU THR ...
TTCACCTTACGGCTCAAGATGAAATTGACG...
1930 1940 1950...
... GLY VAL LYS SER VAL GLU PHE LYS ASP THR
... GCGGTGAAGAGCGGTGGAGTTTAAAGACACG
... 1960 1970 1980

ALA ASN GLY SER ASN GLY ALA SER THR LYS ...
GCGAATGGTTCAACGGGTGCAAGCACGAAG...
1990 2000 2010...
... ILE THR LYS ASP GLY LEU THR ILE THR SER
... ATTACCAAGACGGCTTGACCATTCGTCG
... 2020 2030 2040

ALA ASN GLY ALA ASN GLY ALA ALA THR ...
GCAACGGTGGCGAATGGTGGCGGGCGGACT...
2050 2060 2070...
... ASP ALA ASP LYS ILE LYS VAL ALA SER ASP
... GATGGGACAAAGATTAAAGTGGCTTCAGAC
... 2080 2090 2100

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FIG. 20K

GLY ILE SER ALA GLY ASN LYS ALA VAL LYS ...
GGCATCAGTGGCGGTTAATAAGCGGTTAA...
2110 2120 2130...
... ASN VAL VAL SER GLY LEU LYS PHE GLY
... AACGTTGTGAGCGGACTGAAGAAATTGGT
2140 2150 2160

ASP ALA ASN PHE ASN PRO LEU THR SER ...
GATGCCGAATTTCATAATCCACTGACCAGTTCC...
2170 2180 2190...
... ALA ASP ASN LEU THR LYS GLN TYR ASP
... GCCGACAACCTTAACGAAACAAATATGACGAT
2200 2210 2220

ALA TYR LYS GLY LEU THR ASN LEU ASP GLU ...
GCCATATAAGGCTTGACCAATTGGATGA...
2230 2240 2250...
... LYS GLY ALA ASP LYS GLN THR LEU THR VAL
... AAGGTGGGACAAAGCAAACTCTGACTGTT
2260 2270 2280

ALA ASP ASN THR ALA THR VAL GLY ASP ...
GCCGACAATACTGCCGCCAACCGTGGGCGAT...
2290 2300 2310...

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FIG.20L

SEQUENCE OF THE INVENTION

... LEU ARG GLY LEU GLY TRP VAL ILE SER ALA
... TTGGCGGCTTGGGCTGGGTCATTCTCTGCG 2340
... 2320

ASP LYS THR THR GLY GLU LEU ASN LYS GLU ...
GACAAACACAGGCGAAGTCAATAAGGA... 2350
... 2360
... TYR ASN ALA GLN VAL ARG ASN ALA ASN GLU
... TACAACGCGCAAGTGCGTAACGCCAATGAA 2400
... 2380

VAL LYS PHE LYS SER GLY ASN GLY ILE HIS ...
GTGAATAATTCAGAGCGGCAACGGTATCCAT... 2410
... 2420
... VAL SER GLY LYS THR VAL ASN GLY ARG
... GTTTCGGGTAAACGGTCAACGGTAGGCGC 2460
... 2440

GLU ILE THR PHE GLU LEU ALA LYS ASP GLU ...
GAAATTACTTTTGAAATTGGCTAAGACGA... 2470
... 2480
... ASN ALA ILE ALA PHE GLY TYR GLY SER LYS
... AATGCCATTGCTTTCGGTTATGGCTCAAA 2520
... 2500

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TYR LYS ALA ASN GLY ASP VAL ASP THR GLU ...
TATAAGCCAA TGGAGATGTGATACGGA A... 2710 2720 2730...

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FIG.20N

THESE ARE THE SEQUENCES

... THR VAL THR VAL LYS ASP LYS ASP GLY LYS
... ACCGTAACCGTTAAGGACAAAGACGGTAAA 2760
... 2740 2750

GLU THR THR VAL THR VAL PRO LYS ALA LEU ...
GAGACTACCGTTACTGTTCCTAAGCGTTA... 2780
... GLY ALA THR VAL GLU ASN SER VAL TYR LEU 2790...
... GGGGCTACGGTTGAAACCTCCGTTATTG 2800 2810 2820
... 2800

GLY ASN LYS SER THR ALA THR LYS ASP LYS ...
GGTAATAATCGACTGCGACAAAGATAAG... 2830 2840 2850...
... GLY LYS ASN LEU LYS SER ASP GLY THR ALA
... GGTAATAACCTGAATCTGATGGTACGGCG 2860 2870 2880
... 2860

GLY ASN THR THR THR ALA GLY THR GLY ...
GGTAACACTACAACCTGCTGGCACACGGGT... 2890 2900 2910...
... THR VAL ASN GLY PHE ALA GLY ALA THR ALA
... ACCGTAACCGGCTTTGCCGGGTGCAACGGCG 2920 2930 2940
... 2920

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THE PAT 2949460

FIG.200

HIS GLY ALA VAL SER VAL GLY ALA SER GLY ...
C A C G G T G C G G T T T C T G T C G G C G C A A G C G G C ...
2950
... GLU GLU ARG ARG ILE GLN ASN VAL ALA ALA
... G A G A A A G A C G T A T C C A A A C G T C G C G G C A
2960
... 2980
2990
3000

GLY GLU ILE SER ALA THR SER THR ASP ALA ...
G G C G A A A T T T C C G C C A C T T C C A C C G A T G C G ...
3010
... ILE ASN GLY SER GLN LEU TYR ALA VAL ALA
... A T T A C G G C A G C C A G T T G T A T G C T G T G G C A
3020
... 3040
3050
3060

LYS GLY VAL THR ASN LEU ALA GLY GLN VAL ...
A A G G G T A A C A A A T C T T G C T G G A C A A G T G ...
3070
... ASN LYS VAL GLY LYS ARG ALA ASP ALA GLY
... A A T A A G T G G C A A A C G T G C A G A T G C A G G T
3080
... 3100
3110
3120

THR ALA SER ALA LEU ALA ALA SER GLN LEU ...
A C A G C A A G T G C A T T A G C A G C T T C A C A G T T A ...
3130
3140
3150...

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TABLE PRESENT

FIG.20P

... PRO GLN ALA SER MET PRO GLY LYS SER MET
... CCACAAGCCTCTATGCCAGGTAATCAATG 3170 3180
... 3160

VAL SER ILE ALA GLY SER TYR GLN GLY ...
GTTTCTATTGCGGGAAGTAGTTATCAAGGT... 3200
... GIN ASN GLY LEU ALA ILE GLY VAL SER ARG 3210...
... CAAATGGTTTAGCTATCGGGGTATCACGA 3220 3230 3240
...

ILE SER ASP ASN GLY LYS VAL ILE ILE ARG ...
ATTTCGGATAATGGCAAGTGATTATTCGC... 3250
... LEU SER GLY THR THR ASN SER GIN GLY LYS 3260 3270...
... TTGTCAGGCACAACCAATAGCCAGGTAATA 3280 3290 3300
...

THR GLY VAL ALA GLY VAL GLY TYR GLN ...
ACAGGCGTTGCAGCAGGTTTGGTTACCAG... 3310
... TRP *** 3320 3330...
... TGGTAATAGAAATTCGGGATCCGC 3340 3350
...

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[illegible]

FIG. 21A

NTHi strain M4071 Hia

MET ASN LYS ILE PHE ASN VAL...
 GCGAATTCAATGAAACAATTTTAAGT...
 10 20 30 ...
 ... ILE TRP ASN VAL MET THR GLN THR TRP ALA
 ...TATTGGAAATGTTATGACTCAAACTGGGC
 40 50 60

VAL	VAL	SER	GLU	LEU	THR	ARG	ALA	HIS	THR...
TGTCGTATCTGA	CTCACTCGCGCCACAC...								
80									
... LYS ARG ALA SER ALA THR VAL ALA THR ALA									
...C A A C G T G C C T C C G C A C C G T G G C A C C G C									
... 100 110 120									

VAL	LEU	ALA	THR	LEU	LEU	SER	THR	THR	VAL...
CGT	A	T	T	G	G	C	G	A	C
130									140
									150 ...
									...
									...T
									C
									A
									G
									G
									G
									T
									A
									C
									A
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									G
									A

THR ASN GLY LEU LYS ALA TYR GLY SER THR...
TACAACGGTTGAAAGCTTATGGAAGTAC...
190 200 210 ...

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SEQUENCE

FIG.21B

... ASN ASN PRO ASN PHE ASN ALA ALA GLY ASN
...GAATAATCCGAATTTC AATGCTGCAGGTAA 240
... 220 230

SER ALA THR ASP LEU ALA ARG GIN PHE ASP...
CTCTGCAACTGATTAGCTAGACAGTTTGA... 260
... 270 ...

... GLY ALA TYR ASP GLY LEU LEU ASN LEU ASN
...TGGTGCTTATGACGGTTTATTAAATCTAAA 300
... 280 290

GLU LYS ASP ALA ASN LYS ASN LEU LEU VAL...
TGAAAAGATGCGGAATAAATCTGTGGT... 320
... 310 330 ...

... THR ASP ASP LYS ALA ALA THR VAL GLY ASN
...GACTGATGATAAGCGCGCACCGTAGGCAA 360
... 340 350

LEU ARG LYS LYS LEU GLY TRP VAL LEU SER SER...
TTTGGCTAAATTGGGTTGGGTATTGTCTAG... 380
... 370 390 ...

... LYS ASN GLY THR ARG ASN GLU LYS SER GLN
...TAAACGGCACAGGACGAGAAAGCCA 420
... 400 410

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206121 29E9E660

FIG.21C

GLN VAL LYS HIS ALA ASP GLU VAL LEU PHE...
ACAACTCAAAACACCGGATGAAGTTGTT...
430
... GLU GLY LYS ASP GLY VAL THR VAL THR SER
...TGAAGGCAAGACGGTGTAACGGTTACTTC
440 450 ...
460 470 480

LYS SER GLU ASN GLY LYS HIS THR VAL THR...
CAAACTCGAAACCGGTAAACACCGTTAC...
490 500 510 ...
... PHE THR LEU GLU LYS ASP LEU ASN VAL LYS
...TTTACCCTTGAGAAAGACCCTTAATGTAAA
520 530 540

ASN ALA THR VAL SER ASP LYS LEU SER LEU...
AAACGCACACCGTTAGCGATAAATTATCGCT...
550 560 570 ...
... GLY ALA ASN GLY ASN LYS VAL ASP ILE THR
...TGGTGCAACCGGCAATAAAGTCGATATTAC
580 590 600

SER ASP THR ASN GLY LEU LYS PHE ALA LYS...
CAGTGATACAAACCGGCTTGAAATTGCGAA...
610 620

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TABLE 21 "29E9E660"

FIG.21D

... PRO SER THR ASN GLY GIN ASN GLY ASN VAL
... ACCAAGTACGAATGGTCAAAACGGTAATGT 660
... 640 650

HIS LEU ASN GLY ILE ALA SER THR LEU THR...
TCACTTAAACGGTATTGGCTCTACCTTAAC... 670
... 680 690 ...

... ASP THR ILE THR GLY THR THR LYS SER ALA
... TGACACAAATTACAGGTACAAACAATACTCTGC 720
... 700 710

THR ASN GLY VAL ASP VAL GIN ASN HIS ASN...
AATAATGGTGTAGATGTGCAGAAATCAATA... 730
... 740 750 ...

... ARG ALA ALA SER VAL ALA ASP VAL LEU ASN
... TCGTGCTGCGAGTGTAGCTGATGTATTGAA 780
... 760 770

ALA GLY TRP ASN ILE GIN GLY ASN GLY ALA...
TGCAGGCTGGAAATATTCAAGGCAACGGAGC... 790
... 800 810 ...

... SER VAL ASP PHE VAL ASN THR THR ASP THR
... GAGCGTTGATTTTGTCAATACTACTACGACAC 840
... 820 830

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106121-2929550

FIG.21E

VAL ASP PHE VAL ASN GLY LEU ASN THR ASN...
AGTAGATTTTGTCATAATGGTTTAAATACCAA...
850 860 870 ...
... VAL ASN VAL THR THR ASP THR ALA HIS ASN
...TGTGAACGTTACGACTGATACGGCTCACAA
880 890 900

LYS LYS THR THR VAL ARG VAL ASP VAL THR...
CAAAAGACAACCGTCCGTGTTGATGTAAAC...
910 920 930 ...
... GLY LEU PRO VAL GIN TYR VAL THR GLU ASP
...GGGCTTGCCGGTCCCAATATGTTACGGAGA
940 950 960

GLY GLU THR THR VAL VAL LYS VAL GLY ASN GLU...
CGGCCGAAACCGTTGTGAAAGTGGGCAATGA...
970 980 990 ...
... TYR TYR GLU ALA LYS GIN ASP GLY SER ALA
...GTATTACGAAGCCAAAGCAAGACGGTTCCGGC
1000 1010 1020

ASP MET ASP LYS LYS VAL GLU ASN GLY LYS...
GGATATGGATAAAGTTCGAAATGGCAA...
1030 1040 1050 ...

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FIG. 21F

FIG.21F

... LEU ALA LYS THR LYS VAL LYS LEU VAL SER
...GCTGGCGAAACTAAAGTTAAATTGGTATC 1080
... 1060 1070

ALA ASN GLY THR ASN PRO VAL LYS ILE SER...
GGCAACCGGTACAAATCCGGGTGAAATCAG ... 1100
... ASN VAL ALA ASP GLY THR GLU ASN THR ASP
...CAATGTTGCGGACGGCACCGGAAATACCGA 1140
... 1120 1130

ALA VAL SER PHE LYS GLN LEU LYS ALA LEU...
TGGGTCAGCTTTAAGCAGTTGAAGCCTT ... 1160
... GLN ASP LYS GLN VAL THR LEU SER ALA SER
...GCAAGACAAACAGGTTACGTTAAGTGCGAG 1200
... 1180 1190

ASN ALA TYR ALA ASN GLY GLY SER ASP ALA...
CAATGCTTATGCCCAATGGCGGTAGCGATGC ... 1220
... ASP GLY GLY LYS GLY ILE GLN THR LEU SER
...CGACGGCGGCAAGGGAATTCAACTTTAAG 1260
... 1240 1250

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FIG.21G

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ASN GLY LEU ASN PHE LYS PHE LYS SER THR...
CAATGGTTTGAAATTTTAAATTTAAATCCAC...
1270 1280 1290 ...
... ASP GLY GLU LEU LEU ASN ILE LYS ALA GLU
...AGACGGCGAGTTGTTGAATATCAAAAGCAGA
1300 1310 1320

ASN ASP THR VAL THR PHE THR PRO LYS LYS...
AAATGACACGGTTTACCTTTACGCCGAA...
1330 1340 1350 ...
... GLY SER VAL GLN VAL GLY ASP GLY LYS
...AGGTTTCGGTCAGGTTGGCGATGATGGTAA
1360 1370 1380

ALA THR ILE GIN ASP GLY ALA LYS THR THR...
GGCTACGATTCAAGACGGCGCAAAACAAC...
1390 1400 1410 ...
... THR GLY LEU VAL GLU ALA SER GLU LEU VAL
...TACCGGTTTGGTTGAGGCTTCTGAATTGGT
1420 1430 1440

ASP SER LEU ASN LYS LEU GLY TRP LYS VAL...
TGACAGCCCTGAACAATAATGGGTTGGAAAGT...
1450 1460 1470 ...

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FIG.21H

... GLY THR GLY THR ASP GLY GLY THR GLY VAL THR
...GGGCACCGGCACTGACGGCACACAGGAGTGAC 1490
... 1480 1500

ASP GLY THR THR HIS THR ASP THR LEU VAL LYS...
CGATGGCACGCATACCGACACTTTAGTGAA... 1510
... 1520
... SER GLY ASP LYS VAL THR LEU LYS ALA GLY
...GTCGGGCGATAAAGTAACCTTTGAAAGCCGG 1530
... 1540 1550 1560

ASP ASN LEU LYS VAL LYS GLN GLU GLY THR...
CGACAATCTGAAGGTCAACAAGAGGGTAC... 1570
... 1580
... ASN PHE THR TYR ALA LEU LYS ASP GLU LEU
...AAACTTCACTTATGCGCTCAAGATGAATT 1590
... 1600 1610 1620

THR ASP VAL LYS SER VAL GLU PHE LYS ASP...
GACGGACGTGAAGAGCGGTGGAGTTTAAAGA... 1630
... 1640
... THR ALA ASN GLY ALA ASN GLY ALA SER THR
...CAGGGCGAATGGTGCAACCGGTGCAAGCAC 1650
... 1660 1670 1680

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FIG.21I

LYS ILE THR LYS ASP GLY LEU THR ILE THR...
GAAGATTACCAAGAGACGGCTTGACCATTAC...
1690 1700 1710 ...
... PRO ALA ASN GLY ALA GLY ALA ALA GLY ALA
...GCCGGCAACGGGTGCCGGGTGCCGGCAGGTGC
1720 1730 1740

ASN THR ALA ASN THR ILE SER VAL THR LYS...
AAACACTGCAACACCAATTAGCGTAACCAA...
1750 1760 1770 ...
... ASP GLY ILE SER ALA GLY ASN LYS ALA VAL
...AGACGGCATTAGCGCGGGTAAATAAGCAGT
1780 1790 1800

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LYS ASN VAL VAL SER GLY LEU LYS LYS PHE...
TAAACGTTGTGAGCGGACTGAAGAAAT...
1810 1820 1830 ...
... GLY ASP ALA ASN PHE ASP PRO LEU THR SER
...TGGTGATGCCGAATTCGATCCGCTGACTAG
1840 1850 1860

SER ALA ASP ASN LEU THR LYS GLN TYR ASP...
CTAGCCGACAACTTAACGAACAATAATA...
1870 1880 1890 ...

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FIG.21J

... ASN ALA TYR LYS GLY LEU THR ASN LEU ASP
...CAATGCCCTATAAAGGCTTGACCAATCTGGA 1920
... 1900

GLU LYS SER LYS GLY LYS GLN THR PRO THR...
TGAAAAAGTAAAGGCAAGCAACTCCGAC... 1940
... VAL ALA ASP ASN THR ALA ALA THR VAL GLY
...CGTTGCTGACAAATACCGCTGCAACCGTGGG 1980
... 1960

ASP LEU ARG ARG GLY LEU GLY TRP VAL ILE SER...
CGATTTCGCGCGGCTTGCGCTGGGTCTTTC... 2000
... ALA ASP LYS THR LYS GLY GLU LEU ASN LYS
...TGCAAGACAAACCAAGGCGGAATCAATAA 2040
... 2020

GLU TYR ASN ALA GIN VAL ARG ASN ALA ASN...
GGAATACACGCAAGTGGCTAACGCTAA... 2060
... GLU VAL LYS PHE LYS SER GLY ASN GLY ILE
...TGAAAGTGAATTCAGAGCGGCAACGGTAT 2100
... 2080

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FIG. 21K

FIG. 21K

ASN VAL SER GLY LYS THR LEU ASP ASN GLY...
CAATGTTTCCGGTAACAATTTGGATAACGG...
2110 2130 ...
... THR ARG GLU ILE THR PHE GLU LEU ALA LYS
...TACGGCGGAAATTACTTTTGAATTGGCTAA
2140 2150 2160

ASP GLU ASN ALA ILE ALA PHE GLY SER GLY...
AGACGAAATAATGCCATTGCTTTTCGGTTCTGG...
2170 2190 ...
... SER LYS ALA LEU ARG ASP ASN THR VAL ALA
...CTCAAAAGCCCTTGCGCGGATAACACGGTGGC
2200 2210 2220

ILE GLY THR GLY ASN VAL VAL ASN ALA GLU...
AATTGGTACGGGCAACGTTGTGAAATGCGGA...
2230 2250 ...
... LYS SER GLY ALA PHE GLY ASP PRO ASN TYR
...AAAATCTGGTGCAATTCGGCGGATCCGAACTA
2260 2270 2280

ILE GLU ASP LYS ALA GLY GLY SER TYR ALA...
CATCGAAGATAAAGCCGGTGGCAGCTACGC...
2290 2310 ...

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FIG. 21L

FIG. 21L

... PHE GLY ASN ASP ASN ARG ILE THR SER LYS
...TTTCGGTAACGATAACCGTATTACTTCTAA 2340
... 2320 2330

ASN THR PHE VAL LEU GLY ASN SER VAL ASN...
AAACACTTTTGTGTTGGGTAATAGTTTAA... 2350
... 2360 2370 ...
... ALA LYS ARG ASP ALA ASN GLY ASN VAL LEU
...TGC GA AACGTGATGC AAATGGCAATGTACT 2400
... 2380 2390

THR GLU GLU LYS GLU VAL VAL GLY LYS ASP...
GACCGAAGAAAGAAAGTGGTTGGAAAGA... 2410
... 2420 2430 ...
... GLY ALA LYS THR LYS VAL THR VAL PRO GLN
...CGGTGCGAAGACGAAGTAACCGTGCCGCA 2460
... 2440 2450

ALA LEU GLY GLU THR VAL GLU ASN SER VAL...
AGCCTTAGGCGAAGAACCGTAGAAATTCTGT... 2470
... 2480 2490 ...
... TYR LEU GLY ASN ALA SER THR ALA THR LYS
...TTATCTCCTGGTAATGCTTCACTGCCGACAA 2520
... 2500 2510

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FIG.21M

ASP LYS GLY LYS ASN LEU LYS SER ASP GLY...
AGATAAGGGTAAATAACCTGAAATCTGATGG...
2530
... THR ALA GLY ASN THR THR THR ALA GLY ALA
...TACGGCGGTAACTACTACAACTGCTGGCGC
2540 2550 ...
... 2560 2570 2580

THR GLY THR VAL ASN GLY PHE ALA GLY ALA...
AACGGGTACGGTAAACGGCTTTGGCGGTGC...
2590 2600 2610 ...
... THR ALA HIS GLY ALA VAL SER VAL GLY ALA
...AACGGCGCACGGTGCGGTTTCTGTCTGGCGC
2620 2630 2640

SER GLY GLU GLU ARG ARG ILE GLN ASN VAL...
AGTGGCGAAGAAAGACGTATCCAAACGT...
2650 2660 2670 ...
... ALA ALA GLY GLU ILE SER ALA THR SER THR
...CGCGGCAGCGGAATTTCCGCTACTTCCAC
2680 2690 2700

ASP ALA ILE ASN GLY SER GLN LEU TYR ALA...
AGATGCCGATTAAACGGGTAGCCAGTTGTATGC...
2710 2720 2730 ...

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FIG. 21N

FIG. 21N

... VAL ALA LYS GLY VAL THR ASN LEU ALA GLY
...TGTGGCAAAAGGGGTTAACAAACCTTGCTGG 2760
... 2740 2750

GLN VAL ASN LYS VAL GLY LYS ARG ALA ASP...
ACAAAGTGAAATAAAGTGGGCAAAACGTGCAGA... 2770
... 2780 2790 ...

... ALA GLY THR ALA SER ALA LEU ALA ALA SER
...TGCAGGTACAGCAAGTGCAATTAGCGGCTTC 2800
... 2810 2820

GLN LEU PRO GLN ALA SER MET PRO GLY LYS...
ACAGTTACCAACAAGCCCTCTATGCCAGGTAA... 2830
... 2840 2850 ...

... SER MET VAL SER ILE ALA GLY SER SER TYR
...ATCAATGGTTTCTATTGCGGGAAGTAGTTA 2860
... 2870 2880

GLN GLY GLN SER GLY LEU ALA ILE GLY VAL...
TCAAGGTCAAAAGTGGTTTAGCTATCGGGGT... 2890
... 2900 2910 ...

... SER ARG ILE SER ASP ASN GLY LYS VAL ILE
...ATCAAGAAATTTCCGATATATGGCAAGTAGT 2920
... 2930 2940

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FIG. 210

FIG.210

ILE ARG LEU SER GLY THR THR ASN SER GLN...
TATTCGCTTGTCAAGGCACCAACCAATAGCCA...
2950 2960 2970 ...

... GLY LYS THR GLY VAL ALA ALA GLY VAL GLY
...AGGTAAACACAGGCCGTTGCAGCAGGTGTTGG
2980 2990 3000

TYR GLN TRP *** ** ASN SER GLY SER
TTACCAAGTGGTAATAGAAATTCCTGGATCCGC
3010 3020 3030

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[illegible]

FIG. 22A

NTHi strain K9 hia sequence

MET ASN LYS ILE PHE ASN VAL ILE TRP ASN ...
 ATGAACAAATTTTTAAACGTTATTTGGAAT...
 10 20 30...

20 VAL MET THR GLN THR TRP ALA VAL SER

 ... G T T A T G A C T C A A C A C T G G G C T G T C G T A T C T
 ... 40 50 60

GLU LEU THR ARG ALA HIS THR LYS ARG ALA ...
G A C T C A C T C G C G C C C A C C A A C G T G C C ...
70 80 90...

80 90...
 ... SER ALA THR VAL ALA THR ALA VAL LEU ALA
 T CCGCAACCGTGCGGACC GCGCTATTGGCG
 100 110 120

THR GLN LEU SER ALA THR ALA GLU ALA ASN ...
ACGCAGTTGTCTGCAACGGCTGAAGCGAAC...
130 140 150...

140 SER SER ALA SER VAL THR SER ARG LEU ASN
 ...
 ... A G T A G C C T T C T G T T A C G A G T A G G T T G A A T
 160 170 180

VAL TYR GLY ASP THR ASN THR LYS PHE ASN ...
GTTATGGCGATACGAATACTAAATTCAT...
190 200 210...

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FIG. 22B

FIG. 22B

... ALA ALA ASN SER ILE ALA ASP LEU ASN
... GCAGCCAAATAATTCAATAGCAGATTTAAT 240
... 220 230

LYS GLN ASN ASP GLY VAL HIS ASP GLY LEU ...
AAACAATAATGATGGTGTTCACGATGGTTTA... 250
... 260 270...
... LEU ASN LEU ASN GLU ASN GLY ALA ASN LYS
... TAAATCTGAATGAATAACGGTGCGAATAAA 300
... 280

LYS LEU VAL ASP ASP THR ALA ALA ...
AAGCTGTTGGTGGATGACAAATACTGGCGCG... 310
... 320 330...
... THR VAL GLY ASP LEU ARG LYS LEU GLY TRP
... ACCGTAGGCGATTACGTAAATTGGGCTGG 360
... 340 350

VAL VAL SER THR LYS ASN GLY LYS GLU ASN ...
GTCGTATCAACCAAAATGGCAAGGAAAT... 370
... 380 390...
... GLU LYS SER GLN VAL LYS GLN ALA ASP
... GAGAAAGCCACACAGTCAACAGCGGAT 420
... 400 410

TABLET 2999660

FIG.22C

GLU VAL LEU PHE LYS GLY SER LYS GLY GLY ...
GAAGTGTGTTTAAAGGCCAGCAAGGCGGT...
430 440 450...

... VAL GLN VAL THR SER THR SER GLU ASN GLY
... GTGCAGGTACTTCCACCCTCTGAAACGGC
460 470 480

LYS HIS ALA ILE THR PHE ALA LEU ALA LYS ...
AACACGCCATTACCTTTGCTTTAGCGAA...
490 500 510...

... ASP LEU ASP MET ARG THR ALA THR VAL SER
... GACCTTGATATGAGAACTGCCGACTGTGAGT
520 530 540

ASP THR LEU THR ILE GLY SER THR THR ...
GATACCTTAACGATTGGCGGTTAGTACT...
550 560 570...

... THR GLY SER ALA THR THR PRO LYS VAL ASN
... ACAGGTAGTGCAACAACCAAGTGAAT
580 590 600

VAL THR SER THR ALA SER GLY LEU ASN PHE ...
GTGACTAGCAGCGCAAGCGGCTTGAACTTT...
610 620 630...

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FIG. 22D

FIG. 22D

... ALA LYS GLY ALA THR GLY ALA ASN GLY ASP
... GCGAAAGGCGCTACAGGTGCTAATGGCGAT 660
... 640 650

THR THR VAL HIS LEU THR ASN ILE ALA SER ...
ACTACGGTTCACTTGACTAATAATTGCTTCA... 680
... THR LEU GIN ASP THR LEU LEU ASN THR GLY
... ACTTTGCAAGATACTCTATTGAAATACTGGG 720
... 700 710

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VAL VAL SER LYS LEU ASP GLY ASN GLY ILE ...
GTTGTGAGTAAATTAGATGGTAATGGTATT... 740
... THR ALA ASP GLU LYS LYS ARG ALA ALA SER
... ACTGCTGACGAGAAACCGTGCGGCAAGC 780
... 760 770

VAL GLN ASP VAL LEU ASN SER GLY TRP ASN ...
GTTCAAGATGTTTAAATAAGTGGTTGGAAT... 800
... ILE LYS GLY VAL LYS THR GLY ALA THR THR
... ATCAAGGGTGTTAAACACAGGTGCGGCAAGC 840
... 820 830

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FIG. 22E

FIG.22E

SER	ASP	ASN	VAL	ASP	PHE	VAL	ARG	THR	TYR	...										
TCT	GAT	AAC	GTT	GAT	TTT	TGT	CCT	ACT	TAC	...	850									
...	860									
...	870									
...	880									
...	890									
...	900									
GLU	THR	THR	LEU	VAL	THR	VAL	ASP	SER	GLU	...										
GAA	ACT	AAC	TGG	TAC	AGT	GGA	TAG	TGA	AA	...	910									
...	920									
...	930									
...	940									
...	950									
...	960									
GLY	ALA	LYS	THR	SER	VAL	ILE	LYS	GLU	LYS	...										
GGT	GGA	AAG	ACC	TCT	GTT	TAT	CAA	GAA	AA	...	970									
...	980									
...	990									
...	1000									
...	1010									
...	1020									
LYS	ASP	THR	ASN	GLN	VAL	ALA	SER	ASN	ASN	...										
AAG	ACA	CAAA	ATCA	AGT	CGC	AAG	TAA	TAA	TAA	...	1030									
...	1040									
...	1050									

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FIG.22F

SEQUENCE "2999654"

... ALA ALA ASP THR ASP GLU GLY LYS GLY
... GCAGCTGATGATACGGATGAGGGCAAGGC
... 1060 1070 1080

LEU VAL THR ALA GLU THR VAL ILE ASN ALA ...
TTAGTCACTGCAGAGACTGTATTCAATGCA...
1090 1100 1110...
... VAL ASN LYS ALA GLY TRP ARG ILE LYS THR
... GTAAACAAGGCTGGTTGGAGAAATTAAACA
... 1120 1130 1140

THR GLY ALA ASN ASN GLN GLY GLN PHE ...
ACGGGTGCTAATAATCAAGCTGGTCAGTTT...
1150 1160 1170...
... GLU THR VAL THR SER GLY THR ASN VAL THR
... GAACTGTCAATCAGGCACAAATGTACC
... 1180 1190 1200

PHE ALA ASP GLY ASN GLY THR ALA VAL ...
TTGCTGATGGCAATGGTACAACTGCAGTC...
1210 1220 1230...
... VAL THR GLY ASP ALA THR ASN GLY ILE THR
... GTAAGTGGCGATGCTACCAATGGTATTACT
... 1240 1250 1260

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FIG. 22G

FIG. 22G

VAL LYS TYR GLU ALA LYS VAL GLY ASP GLY ...
GTTAAATACGAAGCGAAGTTGGCGACGGC...
1270 1280 1290...
... LEU LYS ILE GLY ASN ASP GLN LYS ILE THR
... TTGAAGATTGGTAACGACCAAAATCACT 1300 1310 1320
...
ALA ASP THR THR ALA LEU THR VAL THR GLY ...
GCAGATACGACCGCACTTACTGTGACGGC...
1330 1340 1350...
... GLY LYS VAL THR ALA PRO ASP ALA THR ASN
... GGTAAGTTACTGCCCTGTGATGCAACCAAT 1360 1370 1380
...
GLY LYS LYS LEU VAL ASN ALA SER GLY LEU ...
GGTAAGAACTTGTTAATGCAAGTGGTTTA...
1390 1400 1410...
... ALA ASP ALA LEU ASN LYS LEU SER TRP THR
... GCTGATGCCGTTAAACAATAATTAGTTGGACT 1420 1430 1440
...
ALA LYS ALA GLU ALA ASP THR ALA ASN GLY ...
GCAAGAGCTGAAGCAGATACCTGCTAATGGC...
1450 1460 1470...
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FIG.22H

TTTTT"EEEEEE

... GLY GLU LEU ASP GLY THR ALA ASP GLU LYS
... GCGAGCTTGATGGAACTGCAGATGAA A A
... 1480 1490 1500

GLU VAL LYS ALA GLY GLU THR VAL THR PHE ...
GAGTTAAAGCAGGCGAAACGGTAACCTTT...
1510 1520 1530...
... LYS ALA GLY LYS ASN LEU LYS VAL LYS GLN
... AAGCGGCGAAGAACTTAAAGTGAA A A A
... 1540 1550 1560

ASP GLY ALA ASN PHE THR TYR SER LEU GLN ...
GATGGTGCGAACTTTTACTTATTCACCTGCA A...
1570 1580 1590...
... ASP ALA LEU THR GLY LEU THR SER ILE THR
... GATGCTTTAACAAGGCTTAACGAGCATTACT
... 1600 1610 1620

LEU GLY THR GLY ASN ASN GLY ALA LYS THR ...
TTAGGTACAGGAAATAATGGTGCGAA A A A C T...
1630 1640 1650...
... GLU ILE ASN LYS ASP GLY LEU THR ILE THR
... GAATCAACAAGACGGCTTAACCATCACA
... 1660 1670 1680

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FIG. 221

FIG. 221

PRO ALA ASN GLY ALA GLY ALA ASN ASN ALA ...
CCAGCAAAATGGGTGCGGGTGCAATAATGCA...
1690 1710...
... ASN THR ILE SER VAL THR LYS ASP GLY ILE
... AACACCATCAGCGTAAACCAAGACGGCATT
1720 1730 1740

SER ALA GLY GLY GIN SER VAL LYS ASN VAL ...
AGTGCGGCGGTTCAGTCGGTTAAACGGTT...
1750 1770...
... VAL SER GLY LEU LYS LYS PHE GLY ASP ALA
... GTGAGCGGACTGAAGAAATTGGTGATGCCG
1780 1790 1800

ASN PHE ASP PRO LEU THR SER SER ALA ASP ...
AATTCGATCCGCTGACTAGCTCCGCCGAC...
1810 1830...
... ASN LEU THR LYS GIN TYR ASP ALA TYR
... AACTTAACGAACAATAATGACGATGCCATT
1840 1850 1860

LYS GLY LEU THR ASN LEU ASP GLU LYS GLY ...
AAGGCTTGACCAATTGGATGAATAAGGT...
1870 1880 1890...

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FIG. 22J

FIG. 22J

... ALA ASP LYS GLN THR LEU THR VAL ALA ASP
... GCGGACAAAGCAAACTCTGACTGTGCGGAC
... 1900 1910 1920

ASN THR ALA ALA THR VAL GLY ASP LEU ARG ...
AATACTGCCCGCAACCGTGGGCGATTGCGC...
1930 1940 1950...

... GLY LEU GLY TRP VAL ILE SER ALA ASP LYS
... GGC TTGGGCTGGGTCA TTCTGCGGACAA
... 1960 1970 1980

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THR THR GLY GLU LEU ASP LYS GLU TYR ASN ...
ACCACAGGCGAATCGATAGGAATACAC...
1990 2000 2010...

... ALA GLN VAL ARG ASN ALA ASN GLU VAL LYS
... GCGCAAGTGCGTAACGCCAATGAAGTGAA
... 2020 2030 2040

PHE LYS SER GLY ASN GLY ILE ASN VAL SER ...
TTCAAAGCGGCAACGGTATCAATGTTTCC...
2050 2060 2070...

... GLY LYS THR VAL ASN GLY ARG ARG GLU ILE
... GTAAACCTGTCAACGGTAGGCGTGAAATT
... 2080 2090 2100

[illegible]

FIG. 22K

THR PHE GLU LEU ALA LYS GLY GLU VAL ...
 A C T T T G A A T T G G C T A A A G G C G A A G T G G T T ...
 2110 2120 2130 ...
 ... LYS SER ASN GLU PHE THR VAL LYS GLU THR
 ... A A A T C G A A T G A A T T A C T G T C A A A G A A A C C
 ... 2140 2150 2160

 ASN GLY LYS GLU THR SER LEU VAL LYS VAL ...
 A A T G G C A A G G A A A C G A G C C T G G T T A A A G T T ...
 2170 2180 2190 ...
 ... GLY ASP LYS TYR TYR SER LYS GLU ASP ILE
 ... G G C G A T A A A T A T T A C A G C A A A G A G G A T A T T
 ... 2200 2210 2220
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 ASP PRO ALA THR GLY LYS PRO LYS VAL THR ...
 G A C C C A G C A A C C G G T A A A C C G A A A G T T A C A ...
 2230 2240 2250 ...
 ... ASN GLY ASN ALA VAL ALA ALA LYS TYR GLN
 ... A A T G G C A A T G C A G T T G C T G C G A A A T A T C A A
 ... 2260 2270 2280

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FIG.22L

THESE SEQUENCES

... GLY SER SER ASN THR ALA VAL THR LEU THR
... GGCAGCAGCAATACCGCTGTACCCCTAACCC 2340
... 2320

ASN LYS GLY TYR GLY TYR VAL THR GLY ASN ...
AACAAAGGTTATGGCTATGTACAGGTATAC... 2350
... 2360

... GIN VAL ALA ASP ALA ILE ALA LYS SER GLY
... CAGTGGCAGATGCCGATTGCCGAAATCAGGC 2400
... 2380

PHE GLU LEU GLY LEU ALA ASP ALA GLU LYS ...
TTTGAGCTTGGTTTGGCTGTATGCCAGAA... 2410
... 2420

... ALA LYS ALA ALA PHE GLY GLY ASP GLU THR LYS
... GCGAAAGCTGCCGTTTGGCGATGAACAAAA 2460
... 2440

ALA LEU SER SER ASP LYS LEU GLU THR VAL ...
GCC TTGCTTCTGTATAATTGGAAACCCGTA... 2470
... 2480

... ASN ALA ASN ASP LYS VAL ARG PHE ALA ASN
... AATGCCAACGACAAAGTCCGTTTTCCTAAT 2520
... 2500

FIG. 22M

FIG. 22M

GLY LEU ASN THR LYS VAL SER ALA ALA THR ...
GGTTTAAATACCAAGTGAGCGCGCAACG... 2530
... VAL GLU SER ILE ASP ALA ASN GLY ASP LYS ... 2550...
... GTGGAAAGCATCGATGCAAAACGGCGATAAA 2560
... 2570 2580

VAL THR THR THR PHE VAL LYS THR ASP VAL ...
GTGACTACAAACCTTTTGTGAAACCGATGTG... 2590
... GLU LEU PRO LEU THR GIN ILE TYR ASN THR ... 2610...
... GAATTGCCCTTTAACGCAAAATCTACAATACC 2620
... 2630 2640

ASP ALA ASN GLY LYS LYS ILE VAL LYS ASN ...
GATGCAACCGGTAAGAAATCGTTAAAAAT... 2650
... GLY ASP LYS TRP TYR THR LYS ASP ASP ... 2660
... GGCGATAAATGGTATTACACGAAAGATGAC 2670...
... 2680 2690 2700

GLY SER THR ASP MET THR LYS GLU VAL THR ...
GGCTCAACTGATATGACTAAAGAGTTACC... 2710
... 2720 2730...

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FIG.22N

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... LEU GLY ASN VAL ASP SER ASP GLY LYS LYS
... CTTGGCAATGTGGATTTCAGACGGCAAGAAA
... 2740 2750 2760

VAL VAL LYS GLU ASP ASN LYS TRP TYR HIS ...
GTTGTGAAGAGACAAAGTGTTATCAC...
2770 2780 2790...

... VAL LYS SER ASP GLY SER THR ASP LYS THR
... GTTAAATCTGATGGTTCTACGGATAAACA
... 2800 2810 2820

GLN VAL VAL GLU GLU ALA LYS VAL SER THR ...
CAGGTGGTCCGAAGAGCTAAAGTTTCTACCC...
2830 2840 2850...

... ASP GLU LYS HIS VAL VAL SER LEU ASP PRO
... GATGAATAACACGTTGTTCAGCCTTGATCCA
... 2860 2870 2880

ASN ASP GLN SER LYS GLY LYS VAL VAL ...
AATGATCAATCAAAAGGTAAAGGCGTGGTC...
2890 2900 2910...

... ILE ASN MET ALA ASN GLY GLU ILE SER
... ATTAACAATATGGCTAATGGCGAAATTCTT
... 2920 2930 2940

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FIG. 220

FIG.220

ALA THR SER THR ASP ALA ILE ASN GLY SER ...
GCCACTTCCACCGATGCCGATTACGGAGT...
2950 2960 2970...

... GLN LEU TYR ALA VAL ALA LYS GLY VAL THR
... CAGTTGTATGCCCGTGGCAAAAGGGTAACA
... 2980 2990 3000

ASN LEU ALA GLY GIN VAL ASN ASN LEU GLU ...
AACCTTGCTGGACACAGTGAAATAATCTTGAG...
3010 3020 3030...

... GLY LYS VAL ASN LYS VAL GLY LYS ARG ALA
... GGCAAGTGAAATAAAGTGGGCAACCGTGCA
... 3040 3050 3060

ASP ALA GLY THR ALA SER ALA LEU ALA ...
GATGCAGGTACTGCAAGTGCAATTAGCGGCT...
3070 3080 3090...

... SER GIN LEU PRO GIN ALA THR MET PRO GLY
... TCACAGTTACCAACAAGCCACTATGCCAGGT
... 3100 3110 3120

LYS SER MET VAL SER ILE ALA GLY SER ...
AAATCAATGGTTTCTATTGCGGGAAGTAGT...
3130 3140 3150...

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FIG.22P

TTTTTGGGAGG

... TYR GIN GLY GIN ASN GLY LEU ALA ILE GLY
... TATCAAGGTCAAAATGGTTTAGCTATCGGG
... 3160 3170 3180

VAL SER ARG ILE SER ASP ASN GLY LYS VAL ...
GTATCAAGAAATTTCCGATAATGGCAAGTG...
... 3190 3200 3210...
... ILE ILE ARG LEU SER GLY THR ASN SER
... ATTATTCGCTTGTCAAGGCACACCAATAGT
... 3220 3230 3240

GIN GLY LYS THR GLY VAL ALA ALA GLY VAL ...
CAAGGTAAACAACAGGCGTTGCAGCAGGTGT...
... 3250 3260 3270...
... GLY TYR GIN TRP ***
... GGTTACCAGTGGTAATAGAAATCCGGATCC
... 3280 3290 3300

NTHi strain K22 Hia

MET	ASN	LYS	ILE	PHE	ASN...
GCGAATTCAATGAACAAATAATTTTAA...					
10	20
	... VAL ILE TRP ASN ...				
	VAL VAL THR GLN THR TRP VAL				
	...C G T T A T T T G G A A T G T T G T G C T C A A C T T G G G T				
	...	30	40	50	60

VAL	VAL	SER	GLU	LEU	THR	ARG	ALA	HIS...
TGTCGTATCTGAAC TCACTCGGCCA ...								
70	80	90	100	110	120			
... THR LYS CYS ALA SER ALA THR VAL ALA VAL ALA								
...CACCAAATGGCCCTCCGCCAACCGTGGC GGTTGC								

[illegible]

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FIG.23B

GLY LEU ASN ALA TYR GLY ASP THR ASN...
TGGGTTGAATGCTTATGGCGATACTAA...
190 ...
... PHE ASN THR THR ASN ASN SER ILE ALA ASP LEU
...TTTAAATACAAACCAATAATTTCGATAGCAGATT
... 210 220 230 240

GLU LYS HIS VAL GIN ASP ALA TYR LYS...
GGAAACACACGTTCAAGATGCTTATAA...
250 ...
... GLY LEU LEU ASN LEU ASN GLU LYS ASP THR ASN
...AGGCTTATTAAATCTGAATGAATAAGATACAAA
... 270 280 290 300

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LYS SER SER PHE LEU VAL ALA ASP ASN...
TAAGTCAAGTTTCTTGGTTGCCGACAA...
310 ...
... THR ALA ALA THR VAL GLY ASN LEU ARG LYS LEU
...TACCGCCGCAACCGTAGGCAATTTCGTAATT
... 330 340 350 360

GLY TRP VAL LEU SER SER LYS ASN GLY...
GGGCTGGGTATTGTCTAGCAAAACGG...
370 380 ...

SEQUENCE

FIG.23C

... THR ARG ASN GLU LYS SER TYR GLN VAL LYS GLN
...CACAAGGAACGAGAAAGCTATCAAGTAAACA
... 390 400 410 420

ALA ASP GLU VAL LEU PHE THR GLY SER...
AGCTGATGAAGTTCTCTTTACTGGATC...
... 430 440

... GLY ALA ALA THR VAL SER SER SER LYS ASP
...TGGTGCTGCAACGGTTAGTTCCAGCTCTAAAGA
... 450 460 470 480

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GLY LYS HIS THR ILE THR ILE SER VAL...
CGGTAAACATACCATTTACCATTTCTGT...
... 490 500

... THR LYS GLY SER PHE ALA GLU VAL LYS THR ASP
...TACCAGGAGTAGTTTGTGCTGAGGTAAACTGA
... 510 520 530 540

ALA THR THR GLY GLY GLN VAL ASN ALA...
TGCAACTACTGGAGGTCAAGTAAACGC...
... 550 560

... ASP ARG GLY LYS VAL LYS ALA GLU ASP GLU ASN
...CGACCGTGGTAAAGTGAAAGCTGAGGACGAGAA
... 570 580 590 600

SEQUENCE 20000000

FIG.23D

GLY ALA ASP VAL ASP LYS LYS VAL ALA...
TGGAGCTGATGTTGATAAGAAAGTTGC ...
610 620

... THR VAL LYS ASP VAL ALA LYS ALA ILE ASN ASP
...A ACTGTAAAGATGTTGCTAAGGCGATTAAACGA
... 630 640 650 660

ALA ALA THR PHE VAL LYS VAL GLU SER...
TGCCGCAACTTTCGTGAAAGTGGAAG ...
670 680

... THR ASP ASP ILE GLU ASN GLY ALA ALA GLY
...CACAGATGATGACATTGAAATAATGGTGCTGCAGG
... 690 700 710 720 101/204

LYS ASN GLU THR THR ASP GLN ALA LEU...
CAAAATGAACCTACAGACCAAGCTCT ...
730 740

... LYS ALA GLY ASP THR LEU THR LEU LYS ALA GLY
...CAAAGCAGGCGACACCTTAACCTTAAAGCGGG
... 750 760 770 780

LYS ASN LEU LYS LYS ALA LYS LEU ASP GLN...
TAAAAACTTAAAGCTAAGTTAGACCA ...
790 800

FIG.23E

... ASN GLY LYS SER VAL THR PHE ALA LEU ALA LYS
...AATGGTAAATCAGTAACCTTTGCTTTAGCGAA 840
... 810 820 830

ASP LEU ASP VAL THR SER ALA LYS VAL...
AGACCTTGATGTGACCTCTGCGAAAGT...

850 860 870 880 890 900
... SER ASP LYS LEU SER ILE GLY LYS ASP THR ASN
...GAGTGATAAGTTGTCTATTGGTAAAGATACGAA

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LYS VAL ASP ILE THR SER ASP ALA ASN...
TAAAGTTGATATTACCAAGTGCAAA...

910 920 930 940 950 960
... GLY LEU LYS LEU ALA LYS THR GLY ASN GLY ASN
...TGGCTTGAAATTGGCGAAACACAGGTACGGAAA

GLY GLN ASN GLY ASN VAL HIS LEU ASN...
TGGTCAAAACGGTAATGTCCTTAA...

970 980 990 1000 1010 1020
... GLY ILE ALA SER THR LEU THR ASP THR ILE THR
...TGGTATTGCTTCGACTTTGACCGATACCATAC

FIG. 23F

FIG.23F

GLY MET THR THR GIN ALA SER ASN GLY...
AGGTATGACACACACAGCAAGCAATGG...
1030
... VAL ALA VAL GIN ASN HIS ASN ARG ALA ALA SER
...CGTGGCTGTGCAGAAATCATATATCGTGCTGCCGAG
1040 1050 1060 1070 1080

VAL ALA ASP VAL LEU ASN ALA GLY TRP...
TGTGGCTGATGTATTATAATGCAGGCTG...
1090
... ASN ILE GIN GLY ASN GLY ALA SER VAL ASP PHE
...GAAATATTCAAGGCAACGAGCGAGCGTTGATTT
1100 1110 1120 1130 1140

VAL ASN ALA TYR ASP THR VAL ASP PHE...
TGTCAATGCTTACGACACAGTAGATT...
1150
... VAL ASN GLY THR ASN THR ASN VAL ASN VAL THR
...TGTCAATGGTACAAACACCAATGTGAACGTAC
1160 1170 1180 1190 1200

THR ASP THR ALA HIS LYS LYS THR THR...
GACTGATACGGCTCACAAAGAACAC...
1210 1220

FIG. 23G

FIG.23G

... VAL ARG VAL ASP VAL THR GLY LEU PRO VAL GLN
...CGTCCGTGTGGATGTAAACAGGCTTGCCGGTTCA 1260
... 1230 1240 1250

TYR VAL THR GLU ASP GLY LYS THR VAL...
ATATGTTACGGAGACGGCAAAACCGT... 1270
... 1280
... VAL LYS VAL ASP ASN LYS TYR TYR GLU ALA LYS 104/204
...TGTGAAGTGGACAATAAGTATTACGAAGCTAA 1320
... 1290 1300 1310

GLN ASP GLY SER ALA ASP MET ASP LYS...
GCAAGACGGTTCGGCGGATATGGATAA... 1330
... 1340
... LYS VAL GLU ASN GLY GLU LEU ALA LYS THR LYS
...AAAGTCGAAATAAGCGAGCTGGCGAATAACCAA 1380
... 1350 1360 1370 1380

VAL LYS LEU VAL SER ALA SER GLY GLN...
AGTGAAATTGGTGTCTGGCAAGCGGTCA... 1390
... 1400
... ASN PRO VAL LYS ILE SER ASN VAL ALA GLU GLY
...AATCCGGTGAAAATCAGCAATGTTCGGGAAGG 1440
... 1410 1420 1430 1440

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FIG.23H

THR GLU GLU THR ALA SER ASP ALA VAL SER PHE...
CACGGAAGAAACGATGCGGTCAGCTT...
1450
... LYS GLN LEU LYS ALA LEU GLN LYS GLN VAL
...TAAGCAATTGAAAGCCCTTGCAAGAGAAACAGGT
1460
... 1470 1480 1490 1500

THR LEU THR THR ALA SER ASN ALA TYR ALA...
TACTTTAACTGCGAGCAATGCTTATGC...
1510
... ASN GLY GLY ASN ASP ALA ASP GLY GLY LYS ALA
...CAATGGTGGTAACGATGCCGACGGCGGCAAGGC
1520
... 1530 1540 1550 1560

THR GLN THR THR LEU ASN GLY LEU ASN...
AACTCAAACTTTAAACAATGTTTGAA...
1570
... PHE LYS PHE LYS SER THR ASP GLY GLU LEU LEU
...TTTAAATTAAATCCACAGACGGCGAGTTGTT
1580
... 1590 1600 1610 1620

ASN ILE LYS VAL GLU ASN ASP THR VAL...
GAACATCAAGTAGAAATGACACAGT...
1630
... 1640

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FIG. 23I

FIG.23I

... THR PHE THR PRO LYS LYS GLY SER VAL GLN VAL
...TACCTTTACGCCGAAAGGTTTCGGTACAGGT 1670
... 1650 1660 1680

GLY GLU ASP GLY LYS ALA THR ILE GLN...
TGGCGAAGACGGTAAGGCTACGATTCA... 1690
... 1700

... ASN GLY THR LYS THR THR ASP GLY LEU VAL GLU
...AATGGTACGAAACCAACCGACGGTTTGGTTGA 1730
... 1710 1720 1740

ALA SER GLU LEU VAL GLU SER LEU ASN...
AGCTTCCGAATTGGTTGAAAGCCTGAA... 1750
... 1760

... LYS LEU GLY TRP LYS VAL GLY VAL ASP LYS ASP
...CAAACTGGGCTGGAAAGTGGGCGTTGATAAAGA 1790
... 1770 1780 1800

GLY SER GLY GLU LEU ASP GLY ALA SER...
CGGCAGCGCGAGCTTGATGGTGCAATC... 1810
... 1820

... ASN GLU THR LEU VAL LYS SER GLY ASP LYS VAL
...CAATGAACCTTTAGTGAGTCCGGCGGATAAAGT 1850
... 1830 1840 1860

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[illegible]

FIG. 23J

THR	LEU	LYS	ALA	GLY	GLU	ASN	LEU	LYS...										
AAC	TGT	GAA	GCG	GAG	AAT	CTG	AAA...											
								1870										
								1880										
								...										
								VAL	LYS	GLN	ASP	GLY	THR	ASN	PHE	THR	TYR	ALA
								...GGT	CACA	AGAC	GCAC	CAACA	ACTTC	ACTTAC	CGC			
								...	1890		1900							1920

[illegible][illegible]

ASN GLY ALA ALA ALA THR ASP ALA ASP...
G A A T G G T G C G G C G C T G A T G C G G A ...
2050 2060 ...

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FIG.23K

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... LYS ILE LYS VAL ALA SER ASP GLY ILE SER ALA
...CAAGATTAAAGTGGCTTCAGACGGCATCAGTGC 2100
... 2070 2080 2090

GLY ASN LYS ALA VAL LYS ASN VAL VAL...
GGGTAAATAAGCGGTTTAAACGTTGT... 2110
... 2120 ...
... SER GLY LEU LYS LYS PHE GLY ASP ALA ASN PHE
...GAGCGGACTGAAGAAATTGGTGATGCGAATT 2150
... 2130 2140 2160

ASN PRO LEU THR SER SER ALA ASP ASN...
CAATCCACTGACCCAGTTCCGCCGACAA... 2170
... 2180 ...
... LEU THR LYS GLN TYR ASP ASP ALA TYR LYS GLY
...CTTAACGAAACAATATGACGATGCCCTATAAAGG 2210
... 2190 2200 2220

LEU THR ASN LEU ASP GLU LYS GLY ALA...
CTTGACCAATTGGATGAAAGGTTGC... 2230
... 2240 ...
... ASP LYS GLN THR LEU THR VAL ALA ASP ASN THR
...GGACAAGCAACTCTGACTGTGCGCAATAC 2270
... 2250 2260 2280

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FIG. 23L

FIG. 23L

ALA ALA THR VAL GLY ASP LEU ARG GLY...
TGCCGCAACCGTGCGCGGATTTCGCGG...
... 2290
... LEU GLY TRP VAL ILE SER ALA ASP LYS THR THR
...CTTGGGCTGGGTCAATTCTGCGGACAAACCAC
... 2310 2320 2330 2340

GLY GLU LEU ASN LYS GLU TYR ASN ALA...
AGCGGAACCTCAATAAGGAATACACGC...
... 2350
... GLN VAL ARG ASN ALA ASN GLU VAL LYS PHE LYS
...GCAAGTGCGTAACGCCCAATGAAGTGAAATTCAA
... 2370 2380 2390 2400

SER GLY ASN GLY ILE HIS VAL SER GLY...
GAGCGCAACGGTATCCATGTTTCGG...
... 2410
... LYS THR VAL ASN GLY ARG ARG GLU ILE THR PHE
...TAAACGGTCAACGGTAGGCGCGAAATTACTTT
... 2430 2440 2450 2460

GLU LEU ALA LYS ASP GLU ASN ALA ILE...
TGAA TTGGCTAAAGACGAAATGCCAT...
... 2470 2480

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FIG.23M

... ALA PHE GLY TYR GLY SER LYS ALA LEU ARG ASP
...TGCTTTCGGTTATGGCTCAAAAGCCTTGCGCGA 2520
... 2490 2500 2510

ASN THR VAL ALA ILE GLY THR GLY ASN...
TAACACGGTGGCAATTGGTACGGGCAA... 2530
... 2540

... VAL VAL ASN ALA GLU LYS SER GLY ALA PHE GLY
...CGTTGTGAATGCGGAAATACTGGTGCAATTCGG 2580
... 2550 2560 2570

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ASP PRO ASN TYR ILE GLU ASP LYS ALA...
CGATCCGAACATACATCGAAGATAAAGC... 2590
... 2600

... GLY GLY SER TYR ALA PHE GLY ASN ASP ASN ARG
...CGGTGGCAGCTACGCTTTCGGTAACGATAACCG 2640
... 2610 2620 2630

ILE THR SER LYS ASN THR PHE VAL LEU...
TATTACTTCTAAACACTTTTGTGTT... 2650
... 2660

... GLY ASN GLY VAL ASN ALA LYS TYR LYS ALA ASN
...GGGTAATGGAGTTAATGCGAAATATAAGCCAA 2700
... 2670 2680 2690

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TABLE 21-29E9E669

FIG.23N

GLY ASP VAL ASP THR GLU THR VAL THR...
TGGAGATGTTGATACGGAACCGTAC...
2710 ...
... VAL LYS ASP LYS ASP GLY LYS GLU THR THR VAL
...CGTTAAGGACAAAGACGGTAAAGAGACTACCGT 2750
... 2730 2740 2760

THR VAL PRO LYS LYS ALA LEU GLY ALA THR...
TACTGTTCCCTAAAGCGTTAGGGCTAC...
2770 ...
... VAL GLU ASN SER VAL TYR LEU GLY ASN LYS SER
...GGTTGAAACCTCCGTTTATTGGGGTAATAATC 2820
... 2790 2800 2810 2820

THR ALA THR LYS LYS ASP LYS GLY LYS ASN...
GACTGCGACAAAGATAGGGGTAA...
2830 ...
... LEU LYS SER ASP GLY THR ALA GLY ASN THR THR
...CCTGAAATCTGATGGTACGGGGGTAACTAC 2880
... 2850 2860 2870 2880

THR ALA GLY THR THR GLY THR VAL ASN...
AACTGCTGGCACAAACGGGTACGGTAA...
2890 ...

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FIG.230

2910 2920 2930 2940 2950 2960 2970 2980 2990 3000 3010 3020 3030 3040 3050 3060 3070 3080 3090 3100 3110 3120

... GLY PHE ALA GLY ALA THR ALA HIS GLY ALA VAL
...CGGCTTTGCCGGTGCAACGGCGCACGGTGCGGT 2940
... 2910 2920 2930

SER VAL GLY ALA SER GLY GLU GLU ARG...
TTCTGTCGGCGCAAGCGCGAAGAAAG... 2950
... 2960
... ARG ILE GLN ASN VAL ALA ALA GLY GLU ILE SER
...ACGTATCCAAACGTCGCGGCAGCGAAATTTC 3000
... 2970 2980 2990

ALA THR SER THR ASP ALA ILE ASN GLY...
CGCCACTTCCACCGATGCGGATTACGG... 3010
... 3020
... SER GLN LEU TYR ALA VAL ALA LYS GLY VAL THR
...CAGCCAGTTGTATGCTGTGGCAAAAGGGGTAC 3060
... 3030 3040 3050

ASN LEU ALA GLY GLN VAL ASN LYS VAL...
AATCTTGCTGGACCAAGTGAAATAAGT... 3070
... 3080
... GLY LYS ARG ALA ASP ALA GLY THR ALA SER ALA
...GGGCAACCGTGCAGATGCAGGTACAGCAAGTGC 3120
... 3090 3100 3110

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FIG.23P

LEU ALA ALA SER GIN LEU PRO GIN ALA...
ATTAGCAGCTTACACAGTTACCAAGC...
3130
... SER MET PRO GLY LYS SER MET VAL SER ILE ALA
...CTCTATGCCAGGTAAATCAATGGTTTCTATTGC
3150 3160 3170 3180

GLY SER SER TYR GIN GLY GIN ASN GLY...
GGGAAGTAGTTATCAAGGTCAAAATGG...
3190
... LEU ALA ILE GLY VAL SER ARG ILE SER ASP ASN
...TTTAGCTATCGGGGTATCAGCAATTTCGGATAA
3210 3220 3230 3240

GLY LYS VAL ILE ILE ARG LEU SER GLY...
TGGCAAGTGATTTATTTCGCTTGTCAGG...
3250
... THR THR ASN SER GIN GLY LYS THR GLY VAL ALA
...CACCAACCAATAGCCAGGTAAACAGGCGTTGC
3270 3280 3290 3300

ALA GLY VAL GLY TYR GIN TRP ***
AGCAGGTGTTGGTTACCAAGTGGTAATA...
3310 3320
...GAATTGATCCGC
... 3330

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H. influenzae type c strain API hia sequence

VAL VAL ARG THR ALA PRO VAL LEU SER PHE ...
GTA GTA CGCACTGCTCCCGTGTGAGCTTC... 210...
190 200

FIG. 24B

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FIG. 24C

FIG. 24C

LEU SER PHE GLY ALA ASN GLY ASP LYS VAL ...
TTATCGTTTGGCGCAACGGCGATAAGTT...
430 440 450...
... ASP ILE THR SER ASP ALA ASN GLY LEU LYS
... GATATTACCAGTGATGCAAAATGGCTTGAAA
460 470 480

LEU ALA LYS THR GLY ASN GLY ASN VAL HIS ...
TTGGCGAAACACAGGTAACGGAAATGTTCA...
490 500 510...
... LEU ASN GLY LEU ASP SER THR LEU PRO ASP
... TTGAATGGTTTGGATTCAACTTGGCTTGAT
520 530 540 550

ALA VAL THR ASN THR GLY VAL LEU SER SER ...
GCGGTAACGAAATACAGGTGTGTTAAGTTCA...
550 560 570...
... SER SER PHE THR PRO ASN ASP VAL GLU LYS
... TCAAGTTTACACCTAATGATGTTGAAAA
580 590 600

THR ARG ALA ALA THR VAL LYS ASP VAL LEU ...
ACAAGAGCTGCAACTGTTAAAGATGTTTA...
610 620 630...

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FIG.24D

SEQUENCE

... ASN ALA GLY TRP ASN ILE LYS GLY ALA LYS
... AATGCAGGTTGGAAACATTAAAGGTGCTAAA 660
... 640 650

THR ALA GLY GLY ASN VAL GLU SER VAL ASP ...
ACTGCTGGAGGTAATGTTGAGAGTGTGAT... 680
... 670 690...
... LEU VAL SER ALA TYR ASN ASN VAL GLU PHE
... TTAGTGTCCTTATAATAATGTTGAAATTT 720
... 700 710

ILE THR GLY ASP LYS ASN THR LEU ASP VAL ...
ATTACAGGCGATAAACAACGCTTGATGT... 740
... 730 750...
... VAL LEU THR ALA LYS GLU ASN GLY LYS THR
... GTATTACAGCTAAAGAAACGGTAACA 780
... 760 770

THR GLU VAL LYS PHE THR PRO LYS THR SER ...
ACCGAAGTGAAATTCAACACCGAACAACCTCT... 800
... 790 810...
... VAL ILE LYS GLU LYS ASP GLY LYS LEU PHE
... GTTATCAAGAAAGACGGTAAGTTATTT 840
... 820 830

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[illegible]

FIG. 24E

THR GLY LYS GLU ASN ASP THR ASN LYS ...
ACTGGAAGAAGAGAAATAACGACACAAATAA...
850 860 870...
... VAL THR SER ASN THR ALA THR ASP ASN THR
... GTACAAAGTAACACGGCGACTGATATAACA
880 890 900

ASP GLU GLY ASN GLY LEU VAL THR ALA LYS ...
GATGAGGGTAATGGCTTAGTCACTGCAAA...
910 920 930...
... ALA VAL ILE ASP ALA VAL ASN LYS ALA GLY
... GCTGTGATTGATGCTGTGAACAAGGCTGGT
940 950 960

TRP ARG VAL LYS THR THR THR ALA ASN GLY ...
TGGAGAGTTAAACAAC TACTGCTAATGGT...
970 980 990...
... GLN ASN GLY ASP PHE ALA THR VAL ALA SER
... CAAATGGCGACTTCGCACTGTGCGTCA
1000 1010 1020

GLY THR ASN VAL THR PHE GLU SER GLY ASP ...
G G C A C A A T G T A C C T T G A A A G T G C G A T ...
1030 1040 1050...

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FIG.24F

THESE ARE THE SEQUENCES

... GLY THR THR ALA SER VAL THR LYS ASP THR
... GGTACAACAGCGTCACTAAGATACT 1080
... 1060 1070

ASN GLY ASN GLY ILE THR VAL LYS TYR ASP ...
AAGGCAATGGCATCTGTTAAGTACGAC... 1100
... ALA LYS VAL GLY ASP GLY LEU LYS PHE ASP
... CGGAAGTTGGCGACGGCTTGAAATTTGAT 1140
... 1120 1130

SER ASP LYS LYS ILE VAL ALA ASP THR ...
AGCGATAAATAATCGTTGCAGATACGACC... 1160
... ALA LEU THR VAL THR GLY LYS VAL ALA
... GCACTTACTGTGACAGGTGGTAAGGTAGCT 1200
... 1180 1190

GLU ILE ALA LYS GLU ASP LYS LYS ...
GAATTGCTAAAGAGATGACAGAAA... 1210
... LEU VAL ASN ALA GLY ASP LEU VAL THR ALA
... CTTGTTAATGCAGGCGGATTTGGTAACAGCT 1260
... 1230 1240 1250

FIG. 24G

FIG. 24G

LEU GLY ASN LEU SER TRP LYS ALA LYS ALA ...
TTAGGTAATCTAAGTTGGAAAGCAAAAGCT...
1270 1280 1290...
... GLU ALA ASP THR ASP THR ASP GLY ALA LEU
... GAGGCTGATACTGATGATACTGATGGTGCGCTT
1300 1310 1320

GLU GLY ILE SER LYS ASP GIN GLU VAL LYS ...
GAGGGGATTTCAAAAGACCAAGAGTCAA...
1330 1340 1350...
... ALA GLY GLU THR VAL THR PHE LYS ALA GLY
... GCAGGCGAAACGGTAACCTTTAAAGCGGGC
1360 1370 1380

LYS ASN LEU LYS VAL LYS GIN ASP GLY ALA ...
AAGAACTTAAAGTGAAACACAGGATGGTGG...
1390 1400 1410...
... ASN PHE THR TYR SER LEU GIN ASP ALA LEU
... AACCTTACTTATTCACCTGCAAGATGCTTTA
1420 1430 1440

THR GLY LEU THR SER ILE THR LEU GLY GLY ...
ACGGGTTTAAACGAGCATTTACTTTAGGTGGT...
1450 1460 1470...

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FIG.24H

SEQUENCE

... THR THR ASN GLY GLY ASN ASP ALA LYS THR
... ACAACTAATGGCGGAAATGATGCGAAAC 1490 1500
...

VAL ILE ASN LYS ASP GLY LEU THR ILE THR ...
GTCAACAACAAGACGGTTTAACCATCAG... 1510 1520
...

... PRO ALA GLY ASN GLY GLY THR THR GLY THR
... CCAGCAGGTAATGGCGGTACGACAGGTACA 1550 1560
...

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ASN THR ILE SER VAL THR LYS ASP GLY ILE ...
AACACCATCAGCGTAACCAAGATGGCAATT... 1570 1580
...

... LYS ALA GLY ASN LYS ALA ILE THR ASN VAL
... AAGCAGGTAATAAGCTATTACTAATGTT 1610 1620
...

ALA SER GLY LEU ARG ALA TVR ASP ALA ...
GCGAGTGGTTTAAGAGCTTATGACGATGCG... 1630 1640
...

... ASN PHE ASP VAL LEU ASN ASN SER ALA THR
... AATTTGATGTTTAAATAAATCTCTGCACT 1670 1680
...

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FIG. 24I

ALA ASP GLU VAL LEU PHE THR GLY ALA GLY ...
GCTGATGAAGTCTCTTACCGGAGCCGGT...
1870 1880 1890...

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FIG.24J

THE "T" OF "TCTT" IS

... ALA ALA THR VAL THR SER LYS SER GLU ASN
... GCTGCTACGGTTACTTCCAAATCTGAAAC 1920
... 1900 1910

GLY LYS HIS THR ILE THR VAL SER VAL ALA ...
GGTAACAATACGATTACCGTTAGTGTGGCT... 1940
... 1930 1950...

... GLU THR LYS ALA ASP SER GLY LEU GLU LYS
... GAAACTAAAGCGGATAGCGGCTTTGAAAAA 1980
... 1960 1970

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ASP GLY ASP THR ILE LYS LEU LYS VAL ASP ...
GATGGCGATACTATTAAAGCTCAAAGTGGAT... 2000
... 1990 2010...

... ASN GLN ASN THR ASP ASN VAL LEU THR VAL
... ATCAAACACTGATAATGTTTAACTGTT 2040
... 2020 2030

GLY ASN ASN GLY THR ALA VAL THR LYS GLY ...
GGTAATAATGGTACTGCTGCTCACTAAAGGT... 2060
... 2050 2070...

... GLY PHE GLU THR VAL LYS THR GLY ALA THR
... GGCTTTGAAACTGTTAAACTGGAGCGACT 2100
... 2080 2090

FIG. 24K

LEU LYS ALA GLY ASP THR LEU THR PHE LYS ...
CTTAAAGCGGGCGATACCTTAACCTTAA...
2290 2300 2310...

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SEQUENCE "PHEBESN"

FIG.24L

... ALA GLY LYS ASN LEU LYS VAL LYS ARG ASP
... GCAGGTAAACCTGAAAGTTAAACGTGAT 2340
... 2320 2330

GLY LYS ASN ILE THR PHE ASP LEU ALA LYS ...
GGAATAATATTACTTTTGACTTGGCGAAA... 2350
... 2360 2370...

... ASN LEU GLU VAL, LYS THR ALA LYS VAL SER
... AACCTTGAGGTGAAACTGCCGAAAGTGAGT 2400
... 2380 2390

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ASP THR LEU THR ILE GLY ASN THR PRO ...
GATACCTTAAACGATTGGCGGGAATACACCT... 2410
... 2420 2430...

... THR GLY GLY THR THR ALA THR PRO LYS VAL
... ACAGGTGGCACTACTGCCGACGCCAAAGTG 2460
... 2440 2450

ASN ILE THR SER THR ALA ASP GLY LEU ASN ...
AATACTACTAGCACGGCTGATGGTTTGAAAT... 2470
... 2480 2490...

... PHE ALA LYS GLU THR ALA ASP ALA SER GLY
... TTGCAAAAGAAACAGCCCGATGCCCTCGGGT 2520
... 2500 2510

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FIG. 24M

FIG. 24M

SER LYS ASN VAL TYR LEU LYS GLY ILE ALA ...
TCTAAGAAATGTTTATTGAAAGGTATTGGCG...
2530
... THR THR LEU THR GLU PRO SER ALA GLY ALA
... ACAACTTTAACTGAGCCCAAGCGGGAGCG
2540
... 2560 2570 2580

LYS SER SER HIS VAL ASP LEU ASN VAL ASP ...
AAGTCTTCACACGTTGATTATAATGTGGAT...
2590
... ALA THR LYS LYS SER ASN ALA ALA SER ILE
... GCGACGAAATAATCCCAATGCAGCAAGTATT
2600 2610... 2620 2630 2640 126/204

GLU ASP VAL LEU ARG ALA GLY TRP ASN ILE ...
GAAGATGTATTGCGCGCAGGTGGAAATATT...
2650
... GLN GLY ASN GLY ASN ASN VAL ASP TYR VAL
... CAAAGTAATGCTAATAATGTTGATTATGTA
2660 2670... 2680 2690 2700

ALA THR TYR ASP THR VAL ASN PHE THR ASP ...
GCGACGTATGACACAGTAACCTTTACCGAT...
2710 2720 2730...

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TABLE 1

FIG.24N

... ASP SER THR GLY THR THR THR VAL VAL
... GACAGCACAGGTACAAACACGGTAACCGTA 2760
... 2740 2750

THR GLN LYS ALA ASP GLY LYS GLY ALA ASP ...
ACCCAAAGCAGATGGCAAAAGGTGCTGAC... 2780
... VAL LYS ILE GLY ALA LYS THR SER VAL ILE 2820
... GTTAAATCGGTGCCGAAACACTTCTGTATC 2810
... 2800

LYS ASP HIS ASN GLY LYS LEU PHE THR GLY ...
AAGACCAACAACGGCAAACTGTTTACAGGC... 2840
... LYS ASP LEU LYS ASP ALA ASN ASN GLY ALA 2880
... AAGACCTGAAGAAGATGCCGAATAATGGTCCA 2870
... 2860

THR VAL SER GLU ASP ASP GLY LYS ASP THR ...
ACCGTTAGTGAAAGATGATGGCAAGACAC... 2900
... GLY THR GLY LEU VAL THR ALA LYS THR VAL 2940
... GGCAACAGGCTTAGTTACTGCAAAACTGTG 2930
... 2920

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FIG.240

ILE ASP ALA VAL ASN LYS SER GLY TRP ARG ...
ATTGATGCAGTAATAAAGCGGTGGAGG...
2950 2960 2970...
... VAL THR GLY GLU GLY ALA THR ALA GLU THR
... GTAAACCGGTGAGGCGCGACTGCCGAAC 2980 2990 3000

GLY ALA THR ALA VAL ASN ALA GLY ASN ALA ...
GGTGCAACCGCGTGAAATGCGGGTAACGCT...
3010 3020 3030...
... GLU THR VAL THR SER GLY THR SER VAL ASN
... GAACCGTTACATCAGGCACGAGCGTGAAC 3040 3050 3060

PHE LYS ASN GLY ASN ALA THR THR ALA THR ...
TTCAAAACCGGCAATGCGGACCAACAGCGACC...
3070 3080 3090...
... VAL SER LYS ASP ASN GLY ASN ILE ASN VAL
... GTAGCAAGATAATGGCAACATCAATGTC 3100 3110 3120

LYS TYR ASP VAL ASN VAL GLY ASP GLY LEU ...
AAATACGATGTAAATGTGTGGTGACGGCTTG...
3130 3140 3150...

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FIG.24P

SEQUENCE

... LYS ILE GLY ASP ASP LYS LYS ILE VAL ALA
... AAGATTGGCCGATGACAAATAATCGTTGCA 3180
... 3170

ASP THR THR THR LEU THR VAL THR GLY GLY ...
GACACGACCACTTACTGTACACAGGTGGT... 3190
... 3200

... LYS VAL SER VAL PRO ALA GLY ALA ASN SER
... AAGGTGCTCTGTTCCCTGCTGGTGCTAATAGT 3240
... 3220

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VAL ASN ASN ASN LYS LYS LEU VAL ASN ALA ...
GTTAATAACAATAAGAACTTGTTAATGCA... 3250
... 3260

... GLU GLY LEU ALA THR ALA LEU ASN ASN LEU
... GAGGGTTTAGCGACTGCTTTTAAACAACCTA 3300
... 3280

SER TRP THR THR ALA LYS ALA ASP LYS TYR ALA ...
AGCTGGACGGCAAAAGCCGATAAATATGCA... 3310
... 3320

... ASP GLY GLU SER GLU GLY GLU THR ASP GLN
... GATGGCGAGTCAGAGGGCGAAACCCGACCAA 3360
... 3340

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FIG. 24Q

FIG.24Q

GLU VAL LYS ALA GLY ASP LYS VAL THR PHE ...
GAAGTCAAGCAGGCGACAAAGTAACCTTT...
3370 3380 3390...
... LYS ALA GLY LYS ASN LEU LYS VAL LYS GLN
... AAGCAGGCAAGAACTTAAAGTGAAACAG
3400 3410 3420

SER GLU LYS ASP PHE THR TYR SER LEU GLN ...
TCTGAAAGAGACTTTACTTTACTTACTGCA...
3430 3440 3450...
... ASP THR LEU THR GLY LEU THR SER ILE THR
... GACACTTTAACAGGCTTACGAGCATTTACT
3460 3470 3480

LEU GLY GLY THR ALA ASN GLY ARG ASN ASP ...
TTAGGTGGTACAGCTAATGGCAGAAATGAT...
3490 3500 3510...
... THR GLY THR VAL ILE ASN LYS ASP GLY LEU
... ACGGGAACCGTCATCAACAAAGACGGCTTA
3520 3530 3540

THR ILE THR LEU ALA ASN GLY ALA ALA ...
ACCATCAGCTGGCAAAATGGTGCTGCGGCA...
3550 3560 3570...

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FIG. 24R

... GLY THR ASP ALA SER ASN GLY ASN THR ILE
... GGCACAGATGCGTCTTAACGGAAACCATC 3600
... 3580 3590

SER VAL THR LYS ASP GLY ILE SER ALA GLY ...
AGTGTAACCAAGACGGCATTAGTGCGGT... 3620
... 3630...
... ASN LYS GLU ILE THR ASN VAL LYS SER ALA
... AATAAGAAATTACCAATGTTAAGAGTGCT 3660
... 3640 3650

LEU LYS THR TYR LYS ASP THR GLN ASN THR ...
TTAAACCTATTAAGATACTCAAAACACT... 3680
... 3690...
... ALA GLY ALA THR GLN PRO ALA ALA ASN THR
... GCAGGTGCAACTCAACCTGCGGCTAATACA 3720
... 3700 3710

ALA GLU VAL ALA LYS GLN ASP LEU VAL ASP ...
GCTGAAGTAGCCAAACAAGACTTGGTTGAT... 3740
... 3750...
... LEU THR LYS PRO ALA THR GLY ALA ALA GLY
... TTAACCTAACCTGCGGACAGGTGCAGCTGGA 3780
... 3760 3770

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FIG.24S

ASN GLY ALA ASP ALA LYS ALA PRO ASP THR ...
AATGGTGCAATGCAAAAGCTCCCGATACC...
3790 3800 3810...
... THR ALA ALA THR VAL GLY ASP LEU ARG GLY
... ACAGCTGCAACCGTAGGCGACTTGCGTGGT
3820 3830 3840

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LEU GLY TRP VAL LEU SER ALA LYS LYS THR ...
TTGGGCTGGGTGCTTTTCAGCTAAGAAACT...
3850 3860 3870...
... ALA ASP GLU THR GLN ASP LYS GLU PHE HIS
... GCAGATGAACAACAAGATTAAGAGTTCCAC...
3880 3890 3900

ALA ALA VAL LYS ASN ALA ASN GLU VAL GLU ...
GCCGCCGTAAACAAACGCAATGAAGTTGAG...
3910 3920 3930...
... PHE VAL GLY LYS ASN GLY ALA THR VAL SER
... TTCGTGGGTAAACACGGTGCAACCGTGCTT
3940 3950 3960

ALA LYS THR ASP ASN ASN GLY LYS HIS THR ...
GCAAAACTGATAACAAACGGAACAATAC...
3970 3980 3990...

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FIG.24T

FIG. 24T 29E9F66D

... VAL THR ILE ASP VAL ALA GLU ALA LYS VAL
... GTAACGATTGATGTTGCAGAGCCAAAGTT
... 4000 4010 4020

GLY ASP GLY LEU LEU LYS ASP THR ASP GLY ...
GGTGATGGTCTTGAAAGATACTGACGGC...
4030 4040 4050...
... LYS ILE LYS LEU LYS VAL ASP ASN THR ASP
... AAGATTAAACTCAAGTAGATAATACAGAT
... 4060 4070 4080

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GLY ASN ASN LEU LEU THR VAL ASP ALA THR ...
GGGAATAATCTATTAAACCGTTGATGCAACA...
4090 4100 4110...
... LYS GLY ALA SER VAL ALA LYS GLY GLU PHE
... AAGGTGCATCCGTTGCCCAAGGGCGAGTTT
... 4120 4130 4140

ASN ALA VAL THR THR ASP ALA THR THR ALA ...
AATGCCGTAAACAACAGATGCAACTACAGCC...
4150 4160 4170...
... GLN GLY THR ASN ALA ASN GLU ARG GLY LYS
... CAGGGCACAAATGCCCAATGAGCGCGGTAAA
... 4180 4190 4200

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TABLE 2000000

FIG.24U

VAL VAL VAL LYS GLY SER ASN GLY ALA THR ...
GTGGTTGTCAAGGGTTCAAAATGGTGCAACT...
4210 4220 4230...
... ALA THR GLU THR ASP LYS LYS VAL ALA
... GCTACCGAAACTGACAAAGAAAGTGCCA
4240 4250 4260

THR VAL GLY ASP VAL ALA LYS ALA ILE ASN ...
ACTGTTGGCGACGTTGCTAAAGCGATTAAAC...
4270 4280 4290...
... ASP ALA ALA THR PHE VAL LYS VAL GLU ASN
... GACGCACTTTCGTGAAAGTGGAATAAT
4300 4310 4320

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ASP ASP SER ALA THR ILE ASP ASP SER PRO ...
GACGACAGTGCTACGATTGATGATAGCCCA...
4330 4340 4350...
... THR ASP GLY ALA ASN ASP ALA LEU LYS
... ACAGATGATGGCGCAATGATGCTCTCAA
4360 4370 4380

ALA GLY ASP THR LEU THR LEU LYS ALA GLY ...
GCAGCGACACCTTGACCTTAAGCGGGT...
4390 4400 4410...

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FIG. 24V

FIG. 24V

... LYS ASN LEU LYS VAL LYS ARG ASP GLY LYS
... AAAA CTTAAAGTTAAACGTTGATGGTAAA
... 4420 4430 4440

ASN ILE THR PHE ALA LEU ALA ASN ASP LEU ...
AATATTACTTTTGCCCTTGCGAACGACCTT...
... 4450 4460 4470...
... SER VAL LYS SER ALA THR VAL SER ASP LYS
... AGTGTA AAAAGCGCAACCGTTAGCGATAAA
... 4480 4490 4500

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LEU SER LEU GLY THR ASN GLY ASN LYS VAL ...
TTATCGCTTGGTACAAACGGCAATAAAGTC...
... 4510 4520 4530...
... ASN ILE THR SER ASP THR LYS GLY LEU ASN
... AATATCACAGCGCACCAAAAGGCTTGAAAC
... 4540 4550 4560

PHE ALA LYS ASP SER LYS THR GLY ASP ASP ...
TTCGCTAAAGATAGTAAGACAGGCGATGAT...
... 4570 4580 4590...
... ALA ASN ILE HIS LEU ASN GLY ILE ALA SER
... GCTAATAATTCACCTTAAATGGCATTTGCTTCA
... 4600 4610 4620

FIG. 24W

FIG. 24W

THR LEU THR ASP THR LEU LEU ASN SER GLY ...
ACTTTAACTGATACATTTGTTAAATAGTGGT...
4630 4640 4650...
... ALA THR THR ASN LEU GLY GLY ASN GLY ILE
... GCGACAAACCAATTAGGTGGTAAATGGTATT
4660 4670 4680

THR ASP ASN GLU LYS LYS ARG ALA ALA SER ...
ACTGATAACGAGAAATAACGCGCGGAGC...
4690 4700 4710...
... VAL LYS ASP VAL LEU ASN ALA GLY TRP ASN
... GTTAAAGATGTCCTTGAAATGCGGGTTGGAAT
4720 4730 4740 136/204

VAL ARG GLY VAL LYS PRO ALA SER ALA ASN ...
GTCGTGGTGTATAACCGGCATCTGCAAT...
4750 4760 4770...
... ASN GLN VAL GLU ASN ILE ASP PHE VAL ALA
... AATCAAGTGGAGAAATATCGACTTTGTAGCA
4780 4790 4800

THR TYR ASP THR VAL ASP PHE VAL SER GLY ...
ACCTACGACACAGTGGAATTTGTTAGTGGA...
4810 4820 4830...

FIG.24X

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... ASP LYS ASP THR THR SER VAL THR VAL GLU
... G A T A A G A C A C C A C G A G T G T A C T G T T G A A 4860
... 4840 4850

SER LYS ASP ASN GLY LYS ARG THR GLU VAL ...
A G T A A G A T A A T G G C A A G A G A C C G A A G T T ... 4880
... LYS ILE GLY ALA LYS THR SER VAL ILE LYS 4890...
... A A A A T C G G T G C G A A G A C T T C T G T T A T C A A A 4900
... 4910 4920

ASP HIS ASN GLY LYS LEU PHE THR GLY LYS ...
G A C C A C A A C G G C A A A C T G T T T A C A G G C A A A ... 4930
... GLU LEU LYS ASP ALA ASN ASN ASN GLY VAL 4940
... G A G C T G A A G G A T G C T A A C A A T A A T G G C G T A 4950...
... 4960 4970 4980

THR VAL THR GLU THR ASP GLY LYS ASP GLU ...
A C T G T T A C C G A A A C C G A C C G C A A A G A C G A G ... 4990
... GLY ASN GLY LEU VAL THR ALA LYS ALA VAL 5000
... G G T A A T G G T T T A G T G A C T G C A A A A G C T G T G 5010...
... 5020 5030 5040

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SEQUENCE

FIG.24Y

ILE ASP ALA VAL ASN LYS ALA GLY TRP ARG ...
ATTGATGCCCGTGAAATAAGGCTGGTTGGAGA...
5050 5060 5070...
... VAL LYS THR THR GLY ALA ASN GLY GLN ASN
... GTTAAACAACAGGTGCTAATGGTCAGAAAT
5080 5090 5100

ASP ASP PHE ALA THR VAL ALA SER GLY THR ...
GATGACTTCGCAACTGTGTCGTCAGGCACA...
5110 5120 5130...
... ASN VAL THR PHE ALA ASP GLY ASN GLY THR
... AATGTAACCTTTGCTGATGGTAATGGCACACA
5140 5150 5160

THR ALA GLU VAL THR LYS ALA ASN ASP GLY ...
ACTGCCGAAGTAACATAAGCAACGACGGT...
5170 5180 5190...
... SER ILE THR VAL LYS TYR ASN VAL LYS VAL
... AGTATTACTGTTAAATACAAATGTTAAAGTGT
5200 5210 5220

ALA ASP GLY LEU LYS LEU ASP GLY ASP LYS ...
GCTGATGGCCTTAAAACTAGACGGCGATAA...
5230 5240 5250...

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FIG. 24Z

FIG. 24Z

... ILE VAL ALA ASP THR THR VAL LEU THR VAL
... ATCGTTGCAGACACGACCGTACTTACTGTG 5280
... 5260 5270

ALA ASP GLY LYS VAL THR ALA PRO ASN ASN ...
GCAGATGGTTAAGTTACAGCTCCGGAATAAT... 5310...
... GLY ASP GLY LYS LYS PHE VAL ASP ALA SER
... GGCGATGGTTAAGAAATTTGTTGATGCCAAGT 5340
... 5320 5330

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GLY LEU ALA ASP ALA LEU ASN LYS LEU SER ...
GGTTAGCGGATGCGTTTAAATAATTAGC... 5370...
... TRP THR ALA THR ALA GLY LYS GLU GLY THR
... TGGACGGCAACTGCTGGTTAAAGAAAGGCACT 5400
... 5380 5390

GLY GLU VAL ASP PRO ALA ASN SER ALA GLY ...
GGTGAAAGTTGATCCTGCAATAATCAGCAGGG... 5430...
... GLN GLU VAL LYS ALA GLY ASP LYS VAL THR
... CAGAGATCAAGCGGGCGGCAAGTAACC 5460
... 5440 5450

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FIG. 24A'

PHE LYS ALA GLY ASP ASN LEU LYS ILE LYS ...
T T T A A G C C G G C G A C A C C T G A A A T C A A A ...
5470 5480 5490 ...
... GIN SER GLY LYS ASP PHE THR TYR SER LEU
... C A A G C G G C A A G A C T T T A C C T A C T C G C T G
5500 5510 5520

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LYS LYS GLU LEU LYS ASP LEU THR SER VAL ...
A A A A G A G C T G A A G A C C T G A C C A G C G T A ...
5530 5540 5550 ...
... GLU PHE LYS ASP ALA ASN GLY GLY THR GLY
... G A G T T C A A A G A C G C A A C G G C G G T A C A G G C
5560 5570 5580

SER GLU SER THR LYS ILE THR LYS ASP GLY ...
A G T G A A G C A C C A A G A T T A C C A A A G A C G C ...
5590 5600 5610 ...
... LEU THR ILE THR PRO ALA ASN GLY ALA GLY
... T T G A C C A T T A C G C C G G C A A C G G T G C G G T
5620 5630 5640

ALA ALA GLY ALA ASN THR ALA ASN THR ILE ...
G C G G C A G G T G C A A C A C A C T G C A A C A C C A T ...
5650 5660 5670 ...

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FIG.24B'

SEQUENCE

... SER VAL THR LYS ASP GLY ILE SER ALA GLY
... AGCGTAACCAAGATGGCATTAGCGGGT 5700
... 5680

ASN LYS ALA VAL THR ASN VAL SER GLY ...
AATAAGCAGTTACAAACGTTGTGAGCGGA... 5710
5720
... LEU LYS LYS PHE GLY ASP GLY HIS THR LEU
... CTGAAGAAATTTGGTGATGGTCATACGTTG 5750
... 5740 5760

ALA ASN GLY THR VAL ALA ASP PHE GLU LYS ...
GCAATGGCACTGTGCTGATTTTGAAAG... 5770
5780
... HIS TYR ASP ASN ALA TYR LYS ASP LEU THR
... CATTATGACCAATGCCCTATAAAGACTTGACC 5810
... 5800 5820

ASN LEU ASP GLU LYS GLY ALA ASP ASN ...
AATTGGATGAAAGAGCGCGGATAATAA... 5830
5840
... PRO THR VAL ALA ASP ASN THR ALA THR
... CCGACTGTGCGGACAAATACCGCTGCAACC 5870
... 5860 5880

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FIG. 24C

FIG. 24C

VAL GLY ASP LEU ARG GLY LEU GLY TRP VAL ...
GTGGGCGATTGCGCGGCTTGGGCTGGGTC...
5890 5900 5910...
... ILE SER ALA ASP LYS THR THR GLY GLU PRO
... ATTCTGCGGACAAACACACAGGCGAACCC
5920 5930 5940

ASN GLN GLU TYR ASN ALA GLN VAL ARG ASN ...
AATCAGGAATACACGCGCAAGTGCGTAAAC...
5950 5960 5970...
... ALA ASN GLU VAL LYS PHE LYS SER GLY ASN
... GCCAATGAAGTGAAATTCAAGAGCGGCAAC
5980 5990 6000

GLY ILE ASN VAL SER GLY LYS THR LEU ASN ...
GGTATCAATGTTTCCGGTAAACATTGAAC...
6010 6020 6030...
... GLY THR ARG VAL ILE THR PHE GLU LEU ALA
... GGTAACGCGGTGATTACCTTTGAAATTGGCT
6040 6050 6060

LYS GLY GLU VAL VAL LYS SER ASN GLU PHE ...
AAGGCGAAGTGGTAAATCGAATGAATT...
6070 6080 6090...

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FIG. 24D

FIG. 24D'

... THR VAL LYS ASN ALA ASP GLY SER GLU THR
... ACCGTTAAGAAATGCCGATGGTTCGGAAACG 6120
... 6100

ASN LEU VAL LYS VAL GLY ASP MET TYR ...
AACTTGGTTTAAAGTTGGCGGATATGTATAC... 6130
... 6140

... SER LYS GLU ASP ILE ASP PRO ALA THR SER
... AGCAAAGAGGATATTGACCCGGCAACCCAGT 6180
... 6160

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LYS PRO MET THR LYS THR GLU LYS TYR ...
AACCGATGACAGGTAATAACTGAAAAATAT... 6200
... 6190

... LYS VAL GLU ASN GLY LYS VAL VAL SER ALA
... AAGGTTGAAACCGGCAAAAGTCGTTCTGCT 6240
... 6220

ASN GLY SER LYS THR GLU THR LEU THR ...
AAGGCAGCAAGACCGAAGTTACCCTAAC... 6250
... 6260

... ASN LYS GLY SER GLY TYR VAL THR GLY ASN
... AACAAAGGTTCCGGCTATGTACAGGTAAAC 6300
... 6280

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1115 P. 1115 2000000000

FIG.24E

GIN VAL ALA ASP ALA ILE ALA LYS SER GLY ...
CAAGTGGCTGATGCCGATTGCCGAAATCAGGC...
6310 6320

... PHE GLU LEU GLY LEU ALA ASP ALA ALA GLU
... TTGAGCTTGGTTTGGCTGATGCCGCGCAGAA
6340 6350 6360

ALA GLU LYS ALA PHE ALA GLU SER ALA LYS ...
GCTGAAAGAGCCCTTTGCCAGAAAGCGCAAA...
6370 6380 6390

... ASP LYS LYS LEU SER LYS ASP LYS ALA GLU
... GACAAGCAATTGCTCTAAAGATAAAGCGGAA
6400 6410 6420

THR VAL ASN ALA HIS ASP LYS VAL ARG PHE ...
ACTGTAAATGCCCAACGATATAAGTCCGTTT...
6430 6440 6450

... ALA ASN GLY LEU ASN THR LYS VAL SER ALA
... GCTAATGGTTTAAATACCAAGTGAAGCGCG
6460 6470 6480

ALA THR VAL GLU SER THR ASP ALA ASN GLY ...
GCAACGGTGGAAGCACTGATGCCAAACGGC...
6490 6500 6510

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FIG. 24F' 2555550

FIG. 24F'

... ASP LYS VAL THR THR THR PHE VAL LYS THR
... GATAAAGTGACCAACCTTTGTGAAACC 6540
... 6520 6530

ASP VAL GLU LEU PRO LEU THR GIN ILE TYR ...
GATGTGGAATTGCCCTTTAACGCAATCTAC... 6550
... 6560 6570...

... ASN THR ASP ALA ASN GLY ASN LYS ILE VAL
... AATACCGATGCCAAACGGTAATAAGATCGTT 6600
... 6580 6590

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LYS LYS ALA ASP GLY LYS TRP TYR GLU LEU ...
AAAAAGCTGACGGGAAAATGGTATGAAC TG... 6610
... 6620 6630...

... ASN ALA ASP GLY THR ALA SER ASN LYS GLU
... AATGCTGATGGTACGGCGAGTAACAAGAA 6660
... 6640 6650

VAL THR LEU GLY ASN VAL ASP ALA ASN GLY ...
GTGACACTTGTTAACGTGATGCAACGGT... 6670
... 6680 6690...

... LYS LYS VAL VAL LYS VAL THR GLU ASN GLY
... AAGAAAGTTGTGAAAGTAACCGGAAATGGT 6720
... 6700 6710

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PCT/CA00/00289

TABLET 299560

FIG.24G'

ALA ASP LYS TRP TYR THR ASN ALA ASP ...
GCGGATAAGTGGTATTACACCAATGCTGAC...
6730 6750...
... GLY ALA ALA ASP LYS THR LYS GLY GLU VAL
... GGTGCTGCGGATATAAACCAAGGCGAAGTG
6760 6770 6780

SER ASN ASP LYS VAL SER THR ASP GLU LYS ...
AGCAATGATAAAGTTTCTTACCGATGAA...
6790 6810...
... HIS VAL VAL ARG LEU ASP PRO ASN ASN GLN
... CACGTTGTCGCGCTTGATCCGAACAATCAA
6820 6830 6840

SER ASN GLY LYS GLY VAL VAL ILE ASP ASN ...
TCGAACGGCAAGGCGTGCTCATTTGACAA...
6850 6870...
... VAL ALA ASN GLY GLU ILE SER ALA THR SER
... GTGGCTAATGGCGGAATTTCTGCCACTTCC
6880 6900

THR ASP ALA ILE ASN GLY SER GIN LEU TYR ...
ACCGATGCGATTAAACGGAAGTCAGTTGTAT...
6910 6930...

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FIG. 24H

FIG. 24H'

... ALA VAL ALA LYS GLY VAL THR ASN LEU ALA
... GCCGTGGCAAAGGGGTAAACAACCTTGCT
... 6940 6950 6960

GLY GLN VAL ASN LEU GLU GLY LYS VAL ...
GGACAAGTGATAATCTTGAGGGCAAAGTG...
6970 6980 6990...
... ASN LYS VAL GLY LYS ARG ALA ASP ALA GLY
... AATAAGTGGGCAACCGTGCAGATGCAGGT
... 7000 7010 7020

THR ALA SER ALA LEU ALA SER GLN LEU ...
ACAGCAAGTGCAATTAGCGGCTTCACAGTTA...
7030 7040 7050...
... PRO GLN ALA THR MET PRO GLY LYS SER MET
... CCACAAGCCACTATGCCAGGTAAATCAATG
... 7060 7070 7080

VAL ALA ILE ALA GLY SER TYR GLN GLY ...
GTTGCTATTGCGGGAAGTAGTTATCAAGGT...
7090 7100 7110...
... GLN ASN GLY LEU ALA ILE GLY VAL SER ARG
... CAAATGGTTTAGCTATCGGGGTATCAAGA
... 7120 7130 7140

[illegible]

FIG. 24I'

```

ILE SER ASP A T G G C A A A G T G A T T A T T C G C ...
A T T C C G A T A T G G C A A A G T G A T T A T T C G C ...
7150
... LEU SER GLY THR THR ASN SER GLN GLY LYS
... T G T C A G G C A C A C C A A T A G T C A G G T A A A
7180
...
7200

```

[illegible]

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FIG.25A

NTHi strain 12 hia locus

TTCTTTT TTTCTTT

TYR TYR HIS TRP *** PRO THR PRO ...
GAATTCTATTACCACTGGGTAAACCAACCT ...
10 20 30 ...

... ALA ALA THR PRO GLU THR ALA GIN GIN ILE
...GCTGCAACGCCAGAAACAGCACAAACAATT
... 40 50 60

HIS TRP LEU HIS GIN PHE THR LYS ALA ARG ...
CACTGGCTACATCAATTACCAAGCTCGC ...
70 80 90 ...

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... ILE GIN TRP ARG LYS THR HIS SER LEU PHE
...ATTCAATGGCGCAAAACCCATTCTTATTCT
... 100 110 120

PHE LYS GLU LYS PRO ASP TYR ALA PHE VAL ...
TTTAAAGAAATAACCCGATTAATGCCCTTTGTG ...
130 140 150 ...

... LEU ALA GLU ASN GLY LYS VAL GIN GLU ILE
...CTGGCAGAAACCGGCAAGTGCAAGAAATC
... 160 170 180

LYS ALA GLU TYR ARG ARG ILE ALA ASN GIN ...
AAGCAGAAATATCGCCGCAATGCCAAATCAA ...
190 200 210 ...

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FIG. 25B

FIG. 25B

... ILE VAL GLU GLU ALA MET ILE ILE ALA ASN
...ATTGGGAAGAGCAATGATTATTGCCCAAC 240
... 220

ILE CYS ALA ALA GLN PHE LEU HIS GLU GLN ...
ATCTGCGCGCCCAATTATTACAGAACAG ...
250 270 ...
... ALA LYS THR GLY ILE PHE ASN ALA HIS SER
...GCAAAACAGGCAATTTCAACGCCACAGC 300
... 280 290

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GLY PHE ASP LYS LYS TYR LEU GLU ASN ALA ...
GGTTTGAATAAATACTTAGAAATGCG ...
310 330 ...
... HIS HIS PHE LEU MET ALA ASN LEU ALA ASN
... 6431.SL (...
...CACCAATTTCTTAATGGCAATTTAGCCAAT 360
... 340 350

GLU GLN ASN GLN THR GLU LEU ALA GLU ARG ...
GAACAATACTCAACTGAAGTGGCAGAACGT ...
370 390 ...
... TYR SER VAL GLU ASN LEU ALA THR LEU ASN
...TATTCAGTAGAAACCTTAGCCAACCTTAAC 420
... 400 410

Case	α	β	γ	δ	ϵ	ζ	η	θ	ι	κ	λ	μ	ν	ξ	\omicron	π	ρ	σ	τ	υ	ϕ	χ	ψ	ω	
1	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0	1.1	1.2	1.3	1.4	1.5	1.6	1.7	1.8	1.9	2.0	2.1	2.2	2.3	2.4	2.5
2	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0	1.1	1.2	1.3	1.4	1.5	1.6	1.7	1.8	1.9	2.0	2.1	2.2	2.3	2.4	2.5
3	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0	1.1	1.2	1.3	1.4	1.5	1.6	1.7	1.8	1.9	2.0	2.1	2.2	2.3	2.4	2.5
4	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0	1.1	1.2	1.3	1.4	1.5	1.6	1.7	1.8	1.9	2.0	2.1	2.2	2.3	2.4	2.5
5	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0	1.1	1.2	1.3	1.4	1.5	1.6	1.7	1.8	1.9	2.0	2.1	2.2	2.3	2.4	2.5
6	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0	1.1	1.2	1.3	1.4	1.5	1.6	1.7	1.8	1.9	2.0	2.1	2.2	2.3	2.4	2.5
7	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0	1.1	1.2	1.3	1.4	1.5	1.6	1.7	1.8	1.9	2.0	2.1	2.2	2.3	2.4	2.5
8	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0	1.1	1.2	1.3	1.4	1.5	1.6	1.7	1.8	1.9	2.0	2.1	2.2	2.3	2.4	2.5
9	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0	1.1	1.2	1.3	1.4	1.5	1.6	1.7	1.8	1.9	2.0	2.1	2.2	2.3	2.4	2.5
10	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0	1.1	1.2	1.3	1.4	1.5	1.6	1.7	1.8	1.9	2.0	2.1	2.2	2.3	2.4	2.5
11	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0	1.1	1.2	1.3	1.4	1.5	1.6	1.7	1.8	1.9	2.0	2.1	2.2	2.3	2.4	2.5
12	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0	1.1	1.2	1.3	1.4	1.5	1.6	1.7	1.8	1.9	2.0	2.1	2.2	2.3	2.4	2.5
13	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0	1.1	1.2	1.3	1.4	1.5	1.6	1.7	1.8	1.9	2.0	2.1	2.2	2.3	2.4	2.5
14	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0	1.1	1.2	1.3	1.4	1.5	1.6	1.7	1.8	1.9	2.0	2.1	2.2	2.3	2.4	2.5
15	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0	1.1	1.2	1.3	1.4	1.5	1.6	1.7	1.8	1.9	2.0	2.1	2.2	2.3	2.4	2.5
16	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0	1.1	1.2	1.3	1.4	1.5	1.6	1.7	1.8	1.9	2.0	2.1	2.2			

FIG. 25C

HIS ARG LEU ILE LYS ALA VAL LEU ALA LYS ...
C A T C G C T T A A T C A A A G C C G T G C T G G C A A A ...
610 620 630 ...

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FIG.25D

SEQUENCE

...	GLN	PRO	TYR	GLU	LYS	PRO	GLN	ASN	ASP	VAL																					
...																															
...	C	A	G	C	C	T	T	A	T	G	A	A	A	A	T	G	A	C	G	T	G	660									
...																					640										
LEU	ALA	ARG	LEU	GLN	GLU	SER	ARG	ARG	GLN	...																					
																					6432.SL										
T	T	G	G	C	A	C	G	T	T	T	G	C	A	A	G	A	G	T	C	T	C	G	C	C	G	C	C	A	A	...	
																													670		
...	ASN	ARG	LEU	VAL	GLU	ARG	ASP	ILE	ALA	ASP																			680		
...																													690		
...	A	T	C	G	C	C	T	A	G	T	G	G	A	A	C	G	T	G	A	T	A	T	T	G	C	C	C	G	A	T	700
...																													710		
TRP	LEU	TYR	CYS	ARG	TYR	LEU	ALA	ASP	LYS	...																				720	
T	G	G	C	T	A	T	T	G	C	C	G	T	T	A	T	C	T	T	G	C	T	G	A	C	A	A	A	...		730	
																													740		
...	VAL	ALA	GLU	ASN	VAL	GLU	PHE	ASN	ALA	GLU																				750	
...	G	T	G	G	C	T	G	A	A	A	T	G	T	G	G	A	T	T	A	A	T	G	C	A	G	A	A	...		760	
...																													770		
VAL	GLN	ASP	VAL	MET	ARG	ALA	GLY	LEU	ARG	...																				780	
G	T	G	C	A	G	A	T	G	T	A	A	T	G	C	G	T	G	C	A	G	G	C	T	T	A	C	G	C	...	790	
																													800		
																													810		
																													...		

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FIG.25E

SEQUENCE

... VAL GIN LEU LEU GLU ASN GLY ALA SER LEU
...GTACAACTGCTCGAAATAATGGTGCAATCGCTA 840
... 820 830

PHE ILE PRO ALA ALA THR LEU HIS ASN ASN ...
TTTATTCTCTGCCCGCCACGTTGCAACAAC... 850
... 860 870 ...

... LYS GLU GLU ILE GIN LEU ASN PRO ASP GLU
...AAGAAGAAATACAGCTAAACCCCTGACGAA 900
... 880 890

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LEU ALA LEU TYR ILE LYS GLY GLU ARG THR ...
CTCGCCCTCTATATAAAGGCGCAACGCACT... 910
... 920 930 ...

... TYR LYS ILE GLY ASP ILE VAL LYS VAL LYS
...TACAAATAAGCGGACATTTGTGAAGTGAA 960
... 940 950

LEU THR GLU VAL LYS GLU ALA THR ARG SER ...
CTCACAGAGTGAAAGAGCAACTCGCAGT... 970
... 980 990 ...

... ILE VAL GLY GLU ILE LEU GIN *** LEU PRO
...ATTGTGGCGGAAATACTTCAATAATTGCC 1020
... 1000 1010

SUBSTITUTE SHEET (RULE 26)

[illegible]

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FIG.25G

... PHE LYS GLN LEU LYS ALA LEU GLN ASN LYS
...CTTAAGCAGTTGAAAGCCCTTGCAAAACAA 1260
... 1240 1250

GLN VAL THR LEU SER ALA SER ASN ALA TYR...
ACAGGTTACGTTTAGCGCGGAGCAATGCTTA ... 1270
... 1280
... ALA ASN GLY GLY SER ASP ALA ASP VAL GLY
...TGCCCAATGCGCGGTAGCGATGCCGACGTCGG 1320
... 1300 1310

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LYS VAL THR GLN THR LEU SER ASN GLY LEU...
CAGGTAACCTCAAACTTTTAGCAATGGTTT ... 1330
... 1340
... ASN PHE LYS PHE LYS SER THR ASP GLY GLU
...GAATTTTAAATTAAATCCACAGACGGCGGA 1380
... 1360 1370

LEU LEU ASN ILE LYS ALA ASP LYS ASP THR...
GTTGTTGAACATCAAGCAGACAGGACAC ... 1390
... 1400
... VAL THR ILE THR ARG ALA SER GLY ALA ASN
...GGTTACCAATTACCGCGGCAAGCGGTGCGGA 1440
... 1420 1430

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SEQUENCE

FIG.25H

GLY ALA ALA THR ASP ALA ASP LYS ILE...
TGGTGGCGGCGGACTGATGCCGACAAGAT...
1450 1460 1470 ...
... LYS VAL ALA SER ASP GLY ILE SER ALA GLY
...TAAAGTGGCTTCAGACGGCATTAGCGCGGG
1480 1490 1500

ASN LYS ALA VAL LYS ASN VAL ALA GLY...
TAATAAGCAGTTATAAACGTCGCGGCAGG...
1510 1520 1530 ...
... GLU ILE SER ALA THR SER THR ASP ALA ILE
...CGAAATTTCGCGCCACTTCCACCCGATGCGGAT
... (6271.SL 1550 1560

ASN GLY SER GLN LEU TYR ALA VAL ALA LYS...
TAACGGCAGTCAGTTGTATGCCGTTGGCAA...
1570 1580 1590 ...
... GLY VAL THR ASN LEU ALA GLY GLN VAL ASN
...GGGGGTAAACAACCTTGCTGGACAAGTGAA
1600 1610 1620

LYS VAL GLY LYS ARG ALA ASP ALA GLY THR...
TAAGTGGGCAACCGTGCAAGATCGAGGTAC...
1630 1640 1650 ...

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FIG. 25

FIG.25I

... ALA SER ALA LEU ALA ALA SER GIN LEU PRO
...AGCAAGTGCAATTAGCGGCTTCACAGTTACC
... 1660 1670 1680

GLN ALA SER MET PRO GLY LYS SER MET VAL...
ACAAGCCCTCTATGCCCCGGGTAAATCAATGGT...
1700 1710 ...
... SER ILE ALA GLY SER TYR GIN GLY GIN
...TCTATTGCGGGAAGTAGTTATCAAGGTCA
1720 1730 1740

SER GLY LEU ALA ILE GLY VAL SER ARG ILE...
AAGTGGTTTAGCTATCGGGGTATCAAGAAAT...
1750 1760 1770 ...
... SER ASP ASN GLY LYS LEU ILE ILE ARG LEU
...TCCGATAATGGCAAAATTGATTATTGCGCTT
1780 1790 1800

SER GLY THR THR ASN SER GIN GLY LYS THR...
GTCAGGCACACCAATAGCCCAAGGTAAAC...
1810 1820 1830 ...
... GLY VAL ALA ALA GLY VAL GLY TYR GIN TRP
...AGGCGTTGCAAGCAGGTGTTGGTTACCAAGTG
1840 1850 1860

GTAATAGAAATTC
1870

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115121 29292650

FIG.26A

ATG AAC AAA ATT TTT AAC GGT ATT TGG AAT GGT GGT ACT CAA ACT TGG Met Asn Lys Ile Phe Asn Val Ile Trp Asn Val Val Thr Gln Thr Trp 2130 2135 2140	48
GTT GTC GTA TCT GAA CTC ACT CCG ACC CAC ACC AAA TGC GCG TCC GCG Val Val Val Ser Glu Leu Thr Arg Thr His Thr Lys Cys Ala Ser Ala 2145 2150 2155	96
ACC GTG GCG GTT GCG GTA TTG GCA ACC CTG TTG TCC GCA ACG GGT GAG Thr Val Ala Val Ala Val Leu Ala Thr Leu Ser Ala Thr Val Glu 2160 2165 2170 2175	144
GCG AAC AAC AAT ACT CCT GGT ACT ACG AAT AAG TTG AAG GCT TAT GCG GAT Ala Asn Asn Asn Thr Pro Val Thr Asn Lys Leu Lys Ala Tyr Gly Asp 2180 2185 2190	192
GCG AAT TTT AAT TTC ACT AAT AAT TCG ATA GCA GAT GCA GAA AAA CAA Ala Asn Phe Asn Phe Thr Asn Asn Ser Ile Ala Asp Ala Glu Lys Gln 2195 2200 2205	240
GTT CAA GAG CCT TAT AAA GGT TTA TTA AAT CTA AAT GAA AAA AAT GCG Val Gln Glu Ala Tyr Lys Gly Leu Leu Asn Leu Asn Glu Lys Asn Ala 2210 2215 2220	288

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FIG. 26B

FIG. 26B

AGT GAT AAA CTG TTG GTG GAG GAC AAT ACT GCG GCG ACC GTA GGC AAT Ser Asp Lys Leu Leu Val Glu Asp Asn Thr Ala Ala Thr Val Gly Asn 2225 2230 2235	336
TTG CGT AAA TTG GGC TGG GTA TTG TCT AGC AAA AAC GGC ACA AGG AAC Leu Arg Lys Leu Gly Trp Val Leu Ser Ser Lys Asn Gly Thr Arg Asn 2240 2245 2250 2255	384
GAG AAA AGC CAA CAA GTC AAA CAT CCG GAT GAA GTG TTG TTT GAA GGC Glu Lys Ser Gln Gln Val Lys His Ala Asp Glu Val Leu Phe Glu Gly 2260 2265 2270	432
AAA GGC GGT GTG CAG GTT ACT TCC ACC TCT GAA AAC GGC AAA CAC ACC Lys Gly Gly Val Gln Val Thr Ser Thr Ser Glu Asn Gly Lys His Thr 2275 2280 2285	480
ATT ACC TTT GCT TTA GCG AAA GAC CTT GGT GTG AAA ACT GCG ACT GTG Ile Thr Phe Ala Leu Ala Lys Asp Leu Gly Val Lys Thr Ala Thr Val 2290 2295 2300	528
AGT GAT ACC TTA ACG ATT GGC GGT GGT GCT GCA GGT GCT ACA ACA Ser Asp Thr Leu Thr Ile Gly Gly Gly Ala Ala Gly Ala Thr Thr 2305 2310 2315	576

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FIG.26C

ACA CCG AAA GTG AAT GTA ACT AGT ACA ACT GAT GGC TTG AAG TTC GCT Thr Pro Lys Val Asn Val Thr Ser Thr Thr Asp Gly Leu Lys Phe Ala 2320 2325 2330 2335	624
AAA GAT GCT GCG GGT GCT AAT GGC GAT ACT ACG GIT CAC TTG AAT GGT Lys Asp Ala Ala Gly Ala Asn Gly Asp Thr Thr Val His Leu Asn Gly 2340 2345 2350	672
ATT GGT TCA ACC TTG ACA GAC ACG CTT GTG GGT TCT CCT GCT ACT CAT Ile Gly Ser Thr Leu Thr Asp Thr Leu Val Gly Ser Pro Ala Thr His 2355 2360 2365	720
ATT GAC GGA GGA GAT CAA AGT ACG CAT TAC ACT CGT GCA GCA AGT ATC Ile Asp Gly Gly Asp Gln Ser Thr His Tyr Thr Arg Ala Ala Ser Ile 2370 2375 2380	768
AAG GAT GTC TTG AAT GCG GGT TGG AAT ATC AAG GGT GIT AAA GCT GCG Lys Asp Val Leu Asn Ala Gly Trp Asn Ile Lys Gly Val Lys Ala Gly 2385 2390 2395	816
TCA ACA ACT GGT CAA TCA GAA AAT GIC GAT TTT GIT CAT ACT TAC GAT Ser Thr Thr Gly Gln Ser Glu Asn Val Asp Phe Val His Thr Tyr Asp 2400 2405 2410 2415	864

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FIG.26D

ACT GTT GAG TTC TTG AGT GCG GAT ACA GAG ACC ACG ACT GTT ACT GTA Thr Val Glu Phe Leu Ser Ala Asp Thr Glu Thr Thr Val Thr Val 2420 2425 2430	912
GAT AGC AAA GAA AAC CCG AAG ACA ACC GAA GTT AAA ATC GGT GCG AAG Asp Ser Lys Glu Asn Gly Lys Arg Thr Glu Val Lys Ile Gly Ala Lys 2435 2440 2445	960
ACT TCT GTT ATC AAA GAA AAA GAC GGT AAG TTA TTT ACT GGA AAA GCT Thr Ser Val Ile Lys Glu Lys Asp Gly Lys Phe Thr Thr Gly Lys Ala 2450 2455 2460	1008
AAC AAA GAG ACA AAT AAA GTT GAT GGT GCT AAC GCG ACT GAA GAT GCA Asn Lys Glu Thr Asn Lys Val Asp Gly Ala Asn Ala Thr Glu Asp Ala 2465 2470 2475	1056
GAC GAA GCG AAA GGC TTA GTG ACT GCG AAA GAT GTG ATT GAC GCA GTG Asp Glu Gly Lys Gly Leu Val Thr Ala Lys Asp Val Ile Asp Ala Val 2480 2485 2490 2495	1104
AAT AAG ACT GGT TCG AGA ATT AAA ACA ACC GAT GCT AAT GGT CAA AAT Asn Lys Thr Gly Trp Arg Ile Lys Thr Thr Asp Ala Asn Gly Gln Asn 2500 2505 2510	1152

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FIG. 26E

FIG. 26E

GCC GAC TTC GCA ACT GTT GCA TCA GGC ACA AAT GTA ACC TTT GCT AGT Gly Asp Phe Ala Thr Val Ala Ser Gly Thr Asn Val Thr Phe Ala Ser 2515 2520 2525	1200
GGT AAT GGT ACA ACT CCG ACT GTA ACT AAT GGC ACC GAT GGT ATT ACC Gly Asn Gly Thr Thr Ala Thr Val Thr Asn Gly Thr Asp Gly Ile Thr 2530 2535 2540	1248
GTT AAG TAT GAT GCG AAA GTT GGC GAC GGC TTA AAA CTA GAT GGC GAT Val Lys Tyr Asp Ala Lys Val Gly Asp Gly Leu Lys Leu Asp Gly Asp 2545 2550 2555	1296
AAA ATC GCT GCA GAT ACG ACC GCA CTT ACT GTG AAT GAT GGT AAG AAC Lys Ile Ala Ala Asp Thr Thr Ala Leu Thr Val Asn Asp Gly Lys Asn 2560 2565 2570 2575	1344
GCT AAT AAT CCG AAA GGT AAA GTG GCT GAT GTT GCT TCA ACT GAC GAG Ala Asn Asn Pro Lys Gly Lys Val Ala Asp Val Ala Ser Thr Asp Glu 2580 2585 2590	1392
AAG AAA TTG GTT ACA GCA AAA GGT TTA GTA ACA GCC TTA AAC AGT CTA Lys Lys Leu Val Thr Ala Lys Gly Leu Val Thr Ala Leu Asn Ser Leu 2595 2600 2605	1440

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FIG.26F

ACC TGG ACT ACA ACT GCT GCT GAG GCG GAC GGT GGT ACG CTT GAT GGA	1488
Ser Trp Thr Thr Ala Ala Glu Ala Asp Gly Gly Thr Leu Asp Gly	2610 2615 2620
AAT GCA AGT GAG CAA GAA GTT AAA CCG GCG GAT AAA GTA ACC TTT AAA	1536
Asn Ala Ser Glu Gln Glu Val Lys Ala Glu Asp Lys Val Thr Phe Lys	2625 2630 2635
GCA GCG AAG AAC TTA AAA GTG AAA CAA GAG GGT GCG AAC TTT ACT TAT	1584
Ala Gly Lys Asn Leu Lys Val Lys Gln Glu Gly Ala Asn Phe Thr Tyr	2640 2645 2650 2655
TCA CTG CAA GAT GCT TTA ACA GCG TTA ACG AGC ATT ACT TTA GGT ACA	1632
Ser Leu Gln Asp Ala Leu Thr Gly Leu Thr Ser Ile Thr Leu Gly Thr	2660 2665 2670
GGA AAT AAT GGT GCG AAA ACT GAA ATC AAC AAA GAC GCG TTA ACC ATC	1680
Gly Asn Asn Gly Ala Lys Thr Glu Ile Asn Lys Asp Gly Leu Thr Ile	2675 2680 2685
ACA CCA GCA AAT GGT GCG GGT GCA AAT AAT GCA AAC ACC ATC AGC GTA	1728
Thr Pro Ala Asn Gly Ala Gly Ala Asn Asn Ala Asn Thr Ile Ser Val	2690 2695 2700

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FIG.26G

ACC AAA GAC GGC ATT AGT GCG GGC CAG TCG GGT AAA AAC GGT GTC	1776
Thr Lys Asp Gly Ile Ser Ala Gly Gly Ser Val Lys Asn Val Val	
2705 2710 2715	
ACC GGA CTG AAG AAA TTT GGT GAT GCG AAT TTC GAT CCG CTG ACT AGC	1824
Ser Gly Leu Lys Lys Phe Gly Asp Ala Asn Phe Asp Pro Leu Thr Ser	
2720 2725 2730 2735	
TCC GGC GAC AAC TTA ACG AAA CAA AAT GAC GAT GGC TAT AAA GGC TTG	1872
Ser Ala Asp Asn Leu Thr Lys Gln Asn Asp Ala Tyr Lys Gly Leu	
2740 2745 2750	
ACC AAT TTG GAT GAA AAA GGT ACA GAC AAG CAA ACT CCA GGT GTC GGC	1920
Thr Asn Leu Asp Glu Lys Gly Thr Asp Lys Gln Thr Pro Val Val Ala	
2755 2760 2765	
GAC AAT ACC GGC GCA ACC GTG GGC GAT TTG CCG GGC TTG GGC TCG GTC	1968
Asp Asn Thr Ala Ala Thr Val Gly Asp Leu Arg Gly Leu Gly Trp Val	
2770 2775 2780	
ATT TCT GCG GAC AAA ACC ACA GGC GGC TCA ACG GAA TAT CAC GAT CAA	2016
Ile Ser Ala Asp Lys Thr Thr Gly Gly Ser Thr Glu Tyr His Asp Gln	
2785 2790 2795	

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FIG. 26H

FIG. 26H

GTT CCG AAT GCG AAC GAA GIG AAA TTC AAA AGC GGC AAC GGT ATC AAT Val Arg Asn Ala Asn Glu Val Lys Phe Lys Ser Gly Asn Gly Ile Asn 2800 2805 2810 2815	2064
GTT TCC GGT AAA ACG GTC AAC GGT AGG GGT GAA ATT ACT TTT GAA TTG Val Ser Gly Lys Thr Val Asn Gly Arg Arg Glu Ile Thr Phe Glu Leu 2820 2825 2830	2112
GCT AAA GGT GAA GIG GGT AAA TCG AAT GAA TTT ACC GTC AAA GAA ACC Ala Lys Gly Glu Val Val Lys Ser Asn Glu Phe Thr Val Lys Glu Thr 2835 2840 2845	2160
AAT GGA AAG GAA ACG ACC CTG GTT AAA GGT GGC GAT AAA TAT TAC AGC Asn Gly Lys Glu Thr Ser Leu Val Lys Val Gly Asp Lys Tyr Tyr Ser 2850 2855 2860	2208
AAA GAG GAT ATT GAC TTA ACA ACA GGT CAG CCT AAA TTA AAA GAT GGC Lys Glu Asp Ile Asp Leu Thr Thr Gly Gln Pro Lys Leu Lys Asp Gly 2865 2870 2875	2256
AAT ACA GTT GCT GCG AAA TAT CAA GAT AAA GGT GGC AAA GTC GTT TCT Asn Thr Val Ala Ala Lys Tyr Gln Asp Lys Gly Gly Lys Val Val Ser 2880 2885 2890 2895	2304

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FIG.261

GTA ACG GAT AAT ACT GAA GCT ACC ATA ACC AAC AAA GGT TCT GGC TAT Val Thr Asp Asn Thr Glu Ala Thr Ile Thr Asn Lys Gly Ser Gly Tyr 2900 2905 2910	2352
GTA ACA GGT AAC CAA GTG CCA GAT GCG ATT CCG AAA TCA GGC TTT GAG Val Thr Gly Asn Gln Val Ala Asp Ala Ile Ala Lys Ser Gly Phe Glu 2915 2920 2925	2400
CTT GGC TTG GCT GAT GAA GCT GAT GCG AAA CCG GCG TTT GAT GAT AAG Leu Gly Leu Ala Asp Glu Ala Asp Ala Lys Arg Ala Phe Asp Asp Lys 2930 2935 2940	2448
ACA AAA GGC TTA TCT GCT GGT ACA ACG GAA ATT GTA AAT GCG CAC GAT Thr Lys Ala Leu Ser Ala Gly Thr Thr Glu Ile Val Asn Ala His Asp 2945 2950 2955	2496
AAA GTC CGT TTT GCT AAT GGT TTA AAT ACC AAA GTG ACG GCG GCA ACG Lys Val Arg Phe Ala Asn Gly Leu Asn Thr Lys Val Ser Ala Ala Thr 2960 2965 2970 2975	2544
GTG GAA ACG ACC GAT GCA AAC GCG GAT AAA GTG ACC ACA ACC TTT GTG Val Glu Ser Thr Asp Ala Asn Gly Asp Lys Val Thr Thr Phe Val 2980 2985 2990	2592

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FIG.26J

AAA ACC GAT GTG GAA TTG OCT TTA ACG CAA ATC TAC AAT ACC GAT GCA Lys Thr Asp Val Glu Leu Pro Leu Thr Gln Ile Tyr Asn Thr Asp Ala 2995 3000 3005	2640
AAC GGT AAG AAA ATC ACT AAA GTT GTC AAA GAT GGG CAA ACT AAA TGG Asn Gly Lys Lys Ile Thr Lys Val Val Lys Asp Gly Gln Thr Lys Trp 3010 3015 3020	2688
TAT GAA CTG AAT GCT GAC GGT ACG GCT GAT ATG ACC AAA GAA GTT ACC Tyr Glu Leu Asn Ala Asp Gly Thr Ala Asp Met Thr Lys Glu Val Thr 3025 3030 3035	2736
CTC GGT AAC GTG GAT TCA GAC GGC AAG AAA GTT GTG AAA GAC AAC GAT Leu Gly Asn Val Asp Ser Asp Gly Lys Lys Val Val Lys Asp Asn Asp 3040 3045 3050 3055	2784
GGC AAG TCG TAT CAC CCC AAA OCT GAC GGT ACT GCG GAT AAA ACC AAA Gly Lys Trp Tyr His Ala Lys Ala Asp Gly Thr Ala Asp Lys Thr Lys 3060 3065 3070	2832
GGC GAA GTG ACG AAT GAT AAA GTT TCT ACC GAT GAA AAA CAC GTT GTC Gly Glu Val Ser Asn Asp Lys Val Ser Thr Asp Glu Lys His Val Val 3075 3080 3085	2880

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FIG. 26K

FIG. 26K

AGC CTT GAT CCA AAT GAT CAA TCA AAA GGT AAA GGT GTC GTC ATT GAC Ser Leu Asp Pro Asn Asp Gln Ser Lys Gly Lys Gly Val Val Ile Asp 3090 3095 3100	2928
AAT GTG GCT AAT GGC GAT AAT TCT GCC ACT TCC ACC GAT GCG ATT AAC Asn Val Ala Asn Gly Asp Ile Ser Ala Thr Ser Thr Asp Ala Ile Asn 3105 3110 3115	2976
GCA AGT CAG TTG TAT GCT GTG GCA AAA GCG GTA ACA AAC CTT GCT GGA Gly Ser Gln Leu Tyr Ala Val Ala Lys Gly Val Thr Asn Leu Ala Gly 3120 3125 3130 3135	3024
CAA GTG AAT AAT CTT GAG GGC AAA GTG AAT AAA GTG GGC AAA GGT GCA Gln Val Asn Asn Leu Glu Gly Lys Val Asn Lys Val Gly Lys Arg Ala 3140 3145 3150	3072
GAT CCA GGT ACA GCA AGT GCA TTA GCG GCT TCA CAG TTA CCA CAA GCC Asp Ala Gly Thr Ala Ser Ala Leu Ala Ala Ser Gln Leu Pro Gln Ala 3155 3160 3165	3120
ACT ATG CCA GGT AAA TCA ATG GTT GCT ATT GCG GCA AGT AGT TAT CAA Thr Met Pro Gly Lys Ser Met Val Ala Ile Ala Gly Ser Ser Tyr Gln 3170 3175 3180	3168

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FIG. 26L

FIG.26L

GGT CAA AAT	GGT TTA	GCT ATC	GGG GTA	TCA AGA	ATT TCC	GAT AAT	GGC	3216
Gly Gln Asn	Gly Leu	Ala Ile	Gly Val	Ser Arg	Ile Ser	Asp Asn	Gly	
3185								
								3190
								3195
AAA GTG	ATT AIT	CGC TTG	TCA GGC	ACA ACC	AAT AGT	CAA GGT	AAA ACA	3264
Lys Val	Ile Ile	Arg Leu	Ser Gly	Thr Thr	Asn Ser	Gln Gly	Lys Thr	
3200								
								3205
								3210
								3215
GGC GTT	CCA CCA	GGT GGT	TAC CAG	TGG				3294
Gly Val	Ala Ala	Gly Val	Gly Tyr	Gln Trp				
								3220
								3225

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Region	Area (km ²)	Population (1990)	Population (2000)	Population (2010)	Population (2020)	Population (2030)	Population (2040)	Population (2050)	Population (2060)	Population (2070)	Population (2080)	Population (2090)	Population (2100)
North America	24,709,000	307,000,000	312,000,000	317,000,000	322,000,000	327,000,000	332,000,000	337,000,000	342,000,000	347,000,000	352,000,000	357,000,000	362,000,000
South America	17,840,000	367,000,000	372,000,000	377,000,000	382,000,000	387,000,000	392,000,000	397,000,000	402,000,000	407,000,000	412,000,000	417,000,000	422,000,000
Europe	10,180,000	727,000,000	732,000,000	737,000,000	742,000,000	747,000,000	752,000,000	757,000,000	762,000,000	767,000,000	772,000,000	777,000,000	782,000,000
Asia	44,000,000	3,627,000,000	3,672,000,000	3,717,000,000	3,762,000,000	3,807,000,000	3,852,000,000	3,897,000,000	3,942,000,000	3,987,000,000	4,032,000,000	4,077,000,000	4,122,000,000
Africa	30,370,000	727,000,000	732,000,000	737,000,000	742,000,000	747,000,000	752,000,000	757,000,000	762,000,000	767,000,000	772,000,000	777,000,000	782,000,000
Oceania	35,700,000	36,700,000	37,200,000	37,700,000	38,200,000	38,700,000	39,200,000	39,700,000	40,200,000	40,700,000	41,200,000	41,700,000	42,200,000

Alignment of NtHi strain 12 5' ORF with HI1733 from *H. influenzae* strain Rd

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FIG. 27B

FIG. 27B

290 300 310 320 330
LNPDELALYIKGERTYKIGDIVKVKLTVEKATRSIVGEILQ
|||||
LNPDELALYIKGERTYKIGDIVKVKLTVEKATRSIVGEILQ
620 630 640 650 X

; ##cross-references GB:L42023; TIGR:HI1733
; ##note named as homolog to a protein from Escherichia coli
; SUMMARY #length 659 #molecular-weight 75782 #checksum 8365

A64139

MFQINPELLAQLKQIHDSEQVEGWKSTDKAYGFLECDKITYFIAPPSMKAMHGDKIKATIEKQGEKE
QAEPEALIEFMLTRFLAKVRFNKDKKLQVLVHPSINQPIGAQQAQSVKEELOEGDWVAVNLKTHPLRDD
RFFYATINQLICRADDELAFWVTLARHEQSRYPVRGAEPYEMLDKTRTNLTALHFTVIDSESMIMDD
ALYIEPIAQNSTQIGKLVVAIADPTAVIALDSQIEQAKQRCFTNNVLPFGNIPMLPRELSDCLSLIAN
ETRPALVCYIETDLTGNTTAKPHFVSAXVQSKAKLAVNKVSDYLEQALNAWQPEMPETAQQIIMLHQFTK
ARIQWRKTHSLFFKEKPDYAFVLAENGKVEIKAEYRRRIANQIVFEAMLIANICAAQFLHEQAKTIGFNT
HSGFDKFFLENAHNFIMANLANEQNQLTELAEYSVENLAITNGYQQRHDIEPIESDYLEIRLRYLITFA
EFKSELAPHFGLGLEGYATWISPIRKYSIMNHLIKAVLAKQPYEKPQNDV/LARLQEARRQNRVVERDI
ADWLYCRYLADKVASNAEFEEAVQDMFRAGLRVQLLENGASLFTPAATLHNNKEEIQLNPDELALYIKGE
RTYKIGDMVKVKLTVEKATRSIVGEILQ

FIG. 28A

Alignment of *H. influenzae* Hia/Hsf and *M. catarrhalis* 200 kDa proteins

[illegible]

RTAPVLSFHSDEGEGICEKVTENSNGCIYFUNGVLKA-----

FIG.28B

TTTTT*2999666

API
Rd
4223
LES-1

...RTAPVLSFHSDEGEKEVTENMGIYFHNKGVILKA-----
...GTFVKVQSTEDDIEDSAATKDNWQAKAGDTILKA-----
...GSAYAQQKDTKHIAIGEONQPRRSCTAKADGDRAIAIGENANAQGG
...GSAYAQN-NSK-AIFGTTGNNDN---ASASNEASIAIGSLAKAHAN
... * * * * *

GAITLKAGNLIKIKQNTDESINASSFTYSLKKDLTDLTSVATEKLSFGANGKVDITSDANG...
GAITLKAGNLIKIKQ---SINASSFTYSLKKDLTDLTSVATEKLSFGANGKVDITSDANG...
GKN-LKAKLDQCGKSVTFALAKDLVKTAKVSDTLTIGENTPAGCATP---KVSITSTADG...
QAIAIGSSNKTVNG-SSLDKIGTDTGQESIAIGDVKASGDASIAIGSDDLHLLDQHENPK...
QAIAIGGSKPDPNQAANQKAGSHAKGESIAIGDVLAEGDASIAIGSDDLYLDRNSTNSK...
** * * * * *

33
32
29
K22
M4071
11

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Case	Age	Sex	Duration of disease	Initial symptoms	Course	Final diagnosis	Pathological findings
1	45	M	10 years	Headache, vomiting, weight loss	Progressive	Brain tumor	Large, well-circumscribed, solid, grayish-white mass in the right frontal lobe, compressing the lateral ventricle.
2	52	F	5 years	Headache, vomiting, weight loss	Progressive	Brain tumor	Large, well-circumscribed, solid, grayish-white mass in the left frontal lobe, compressing the lateral ventricle.
3	60	M	15 years	Headache, vomiting, weight loss	Progressive	Brain tumor	Large, well-circumscribed, solid, grayish-white mass in the right frontal lobe, compressing the lateral ventricle.
4	65	F	10 years	Headache, vomiting, weight loss	Progressive	Brain tumor	Large, well-circumscribed, solid, grayish-white mass in the left frontal lobe, compressing the lateral ventricle.
5	70	M	10 years	Headache, vomiting, weight loss	Progressive	Brain tumor	Large, well-circumscribed, solid, grayish-white mass in the right frontal lobe, compressing the lateral ventricle.
6	75	F	10 years	Headache, vomiting, weight loss	Progressive	Brain tumor	Large, well-circumscribed, solid, grayish-white mass in the left frontal lobe, compressing the lateral ventricle.
7	80	M	10 years	Headache, vomiting, weight loss	Progressive	Brain tumor	Large, well-circumscribed, solid, grayish-white mass in the right frontal lobe, compressing the lateral ventricle.
8	85	F	10 years	Headache, vomiting, weight loss	Progressive	Brain tumor	Large, well-circumscribed, solid, grayish-white mass in the left frontal lobe, compressing the lateral ventricle.
9	90	M	10 years	Headache, vomiting, weight loss	Progressive	Brain tumor	Large, well-circumscribed, solid, grayish-white mass in the right frontal lobe, compressing the lateral ventricle.
10	95	F	10 years	Headache, vomiting, weight loss	Progressive	Brain tumor	Large, well-circumscribed, solid, grayish-white mass in the left frontal lobe, compressing the lateral ventricle.

FIG. 28C

K9
HSF
API
Rd
4223
LES-1

```

...
...LKLAKTGN--VHLGLDSTLPDAVTNIGVLSSSS-FTPNDEVKTR
...LKLAKTGN--VHLGLDSTLPDAVTNIGVLSSSS-FTPNDEVKTR
...LKLAKGNDPAVHLGLASTLPDVTNIGASTSVT-FSPSDIEKTR
...HPKGTLLNDLJNGHAVLKEIRSSKNDVKYRRTTASCHASTA/GAMS
...YPNGLLSTLIQN-HTVLRQIRDSNGSQ-KYRRTAAEGHASTA/GAMA
*          *          *          *          *          *

```

.....

* * * * *

AATVKDVLNAGANNIKGAKTACQNVESVDLVSAYNNVEFITGDKNITLDVLTAKENGKITEVK
AATVKDVLNAGANNIKGAKTACQNVESVDLVSAYNNVEFITGDKNITLDVLTAKENGKITEVK
AATIKDVLNAGANNIKGAKVACQNTESVDLVAGYTNVEFITGDKNITLDVLTAKENGKITEVK
YAQGHFSAFGTRA-TAKSAYSGLAVLAATAEQSTIATGSDATSSSLGALTAGIRAQLQ
YAKIGHFANAFGRS-TAEENYSKAUGLTAKAEKGTYIATGSNAQAINYCALALGADTRVDLD

* * * * *

33 32 29 K22

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[illegible]

FIG. 28D

```

M4071
11
K9
HSF
API
Rd
4223
IES-1

```

TENTDEENGLVTA KAVI - DAVA KAGWIVKITTANGQNGDEFATVASGINVTESGDTTASVT
TNTDENGVLVTAKAVI--DAVNKAGWIVKTTITANGQNGDEFATVASGINVTESGDTTASVT.
TETIDEMA*

*RYRNGLVTAKTVI-EAVKSGWRVTTTANGQNDDEATVAGINVTFANGTASVT...
SNSIKRKLIINVAGAVKNTDANVAQLEAVVKWAKERRITFQGDINSTDKIGLDNLTIKG...
SSTIKRKLIINVAGAYETDANVAQLKAVENLAK-RQITFKGDINGVGVKKLGEHLTIKG...
* **** * * * * * * * *

33

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32
29
K22
M4071
11
K9
HSF
API
Rd
Rd
4223
LES-1

[illegible]

FIG. 28E

[illegible]

33
32
29
K22
M4071
11
K9
HSF
API
Rd
4223
LES-1

FIG. 28F

TAASEKTVGSENN-TAELOSGLFTT-PTINA-SIDKTVGIDGLKFTXNSN-TALEDTT-R...

[illegible]

60 70

-----ACSTTGINSLVYK-NNSNFNSANSIA.....

-----NN--SV.G.A.A.D--T..TT.....

-----N--SV.G.A.A.D--T..TT.....

-----T.G.S.G.KA.ST.P..A.G..AT.....

-----N--PV.K.KA.D-A.F.--T.....

-----ASV.CR....D-T.TK.A.....

KTVINKDGLTTPAGNGTGTGNIISBTQGIK.NKAI.VASGLRAYDDA.DVL...AT...AT...

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FIG. 28G

FIG. 28G

KIVINKGLTITPAGNGTGTINTISBTKGK..NKAI..VASGLRAYDDA..DVL...AT...
 KIVINKGLTITPAGNGTGTINTISBTKGK..NKAI..VASGLRAYDDA..DVL...AT...

 -----VNNITGGSNKQIQVGADGKIFADVNNVNSNAKFGTITRTEEEIGFAD...
 ** *** * ** ***** * * * * *
 ...80 90 100 110 120
 ...DIANKQNSVYDGLIALNEKGTDSKFLVADETTATVGNLRKL-----
 ...-----ATDENED..EELEPVQRSV...
 ...E.HVQDA.K.....D.N..S.....N.A.....
 ...E.HVQDA.K.....D.N..S.....N.A.....
 ...AR.F.GA.....DAN.N-L..T.DKA.....
 ...AE..VQEA.K.....NAS-D.L..E.N.A..D.....
 ...G.H.....N.AN..-L..D.N.A..D.....
 ...RHVEDA.K.....NAN.QP-..T.S.A..D.....
 ...RHVEDA.K.....NAN.QP-..TDS.A..D.....
 ...RHVEDA.K.....NAN.QP-..S.A..D.....
 ...-----KQAP.LDKKQ.KVGSVAITIDNGI.AGNKIS..A.GSSANDA
 ...CKV/DKK.P.LDKKQ.QVG.VKIT.DSGINAGDQKISNWKDNTDUTDA
 ...* * * * *
 ...* * * * *

33
 32
 29
 K22
 M4071
 11
 K9
 HSF
 API
 Rd
 4223
 LES-1

130 140 150 160
 GWVSTKNSKTEE-SNOVKQADEVLFEK-KDGVIVTSKSENGKHVT-----
 R.SFKSAKEGTG.QEGTTEV-----
 ...L.S..G.RN.K.Y.....T..SGAA..S.S.KD..I..-----
 ...L.S..G.RN.K.Y.....T..SGAA..S.S.KD..I..-----

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Case	Age	Sex	Duration of illness	Onset	Course	Outcome	Remarks
1	20	M	10 years	1950	Chronic	Recovery	First case in the series
2	25	F	5 years	1951	Chronic	Recovery	Second case in the series
3	30	M	3 years	1952	Chronic	Recovery	Third case in the series
4	35	F	2 years	1953	Chronic	Recovery	Fourth case in the series
5	40	M	1 year	1954	Chronic	Recovery	Fifth case in the series
6	45	F	6 months	1955	Chronic	Recovery	Sixth case in the series
7	50	M	4 months	1956	Chronic	Recovery	Seventh case in the series
8	55	F	3 months	1957	Chronic	Recovery	Eighth case in the series
9	60	M	2 months	1958	Chronic	Recovery	Ninth case in the series
10	65	F	1 month	1959	Chronic	Recovery	Tenth case in the series
11	70	M	10 days	1960	Chronic	Recovery	Eleventh case in the series
12	75	F	1 week	1961	Chronic	Recovery	Twelfth case in the series
13	80	M	1 week	1962	Chronic	Recovery	Thirteenth case in the series
14	85	F	1 week	1963	Chronic	Recovery	Fourteenth case in the series
15	90	M	1 week	1964	Chronic	Recovery	Fifteenth case in the series
16	95	F	1 week	1965	Chronic	Recovery	Sixteenth case in the series
17	100	M	1 week	1966	Chronic	Recovery	Seventeenth case in the series
18	105	F	1 week	1967	Chronic	Recovery	Eighteenth case in the series
19	110	M	1 week	1968	Chronic	Recovery	Nineteenth case in the series
20	115	F	1 week	1969	Chronic	Recovery	Twentieth case in the series

FIG. 28H

[illegible]

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[illegible][illegible][illegible]

[illegible]

FIG. 28J

.....

PKWNITSTADGLNFAKETADASGKNVYLGIAITLTPESAGAKSSHVDLNVDA TK-KSNAA...
PKWNITSTADGLNFAKETADASGKNVYLGIAITLTPESAGAKSSHVDLNVDA TK-KSNAA...

PYLPDQKLOQVNWKITNIGINAGCKATGLSPTLPSIADQSS-PNIELGNTI-QQKDKSNA...
 -----GLSPTL(SITNAGVTRTEQGVNITSDEKSKAA...
 * ** * *** * *** * ** * * * * *

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[illegible]

α^0	α^1	α^2	α^3	α^4	α^5	α^6	α^7	α^8	α^9	α^{10}	α^{11}	α^{12}	α^{13}	α^{14}	α^{15}	α^{16}	α^{17}	α^{18}	α^{19}	α^{20}	α^{21}	α^{22}	α^{23}	α^{24}	α^{25}	α^{26}	α^{27}	α^{28}	α^{29}	α^{30}	α^{31}	α^{32}	α^{33}	α^{34}	α^{35}	α^{36}	α^{37}	α^{38}	α^{39}	α^{40}	α^{41}	α^{42}	α^{43}	α^{44}	α^{45}	α^{46}	α^{47}	α^{48}	α^{49}	α^{50}	α^{51}	α^{52}	α^{53}	α^{54}	α^{55}	α^{56}	α^{57}	α^{58}	α^{59}	α^{60}	α^{61}	α^{62}	α^{63}	α^{64}	α^{65}	α^{66}	α^{67}	α^{68}	α^{69}	α^{70}	α^{71}	α^{72}	α^{73}	α^{74}	α^{75}	α^{76}	α^{77}	α^{78}	α^{79}	α^{80}	α^{81}	α^{82}	α^{83}	α^{84}	α^{85}	α^{86}	α^{87}	α^{88}	α^{89}	α^{90}	α^{91}	α^{92}	α^{93}	α^{94}	α^{95}	α^{96}	α^{97}	α^{98}	α^{99}	α^{100}	α^{101}	α^{102}	α^{103}	α^{104}	α^{105}	α^{106}	α^{107}	α^{108}	α^{109}	α^{110}	α^{111}	α^{112}	α^{113}	α^{114}	α^{115}	α^{116}	α^{117}	α^{118}	α^{119}	α^{120}	α^{121}	α^{122}	α^{123}	α^{124}	α^{125}	α^{126}	α^{127}	α^{128}	α^{129}	α^{130}	α^{131}	α^{132}	α^{133}	α^{134}	α^{135}	α^{136}	α^{137}	α^{138}	α^{139}	α^{140}	α^{141}	α^{142}	α^{143}	α^{144}	α^{145}	α^{146}	α^{147}	α^{148}	α^{149}	α^{150}	α^{151}	α^{152}	α^{153}	α^{154}	α^{155}	α^{156}	α^{157}	α^{158}	α^{159}	α^{160}	α^{161}	α^{162}	α^{163}	α^{164}	α^{165}	α^{166}	α^{167}	α^{168}	α^{169}	α^{170}	α^{171}	α^{172}	α^{173}	α^{174}	α^{175}	α^{176}	α^{177}	α^{178}	α^{179}	α^{180}	α^{181}	α^{182}	α^{183}	α^{184}	α^{185}	α^{186}	α^{187}	α^{188}	α^{189}	α^{190}	α^{191}	α^{192}	α^{193}	α^{194}	α^{195}	α^{196}	α^{197}	α^{198}	α^{199}	α^{200}	α^{201}	α^{202}	α^{203}	α^{204}	α^{205}	α^{206}	α^{207}	α^{208}	α^{209}	α^{210}	α^{211}	α^{212}	α^{213}	α^{214}	α^{215}	α^{216}	α^{217}	α^{218}	α^{219}	α^{220}	α^{221}	α^{222}	α^{223}	α^{224}	α^{225}	α^{226}	α^{227}	α^{228}	α^{229}	α^{230}	α^{231}	α^{232}	α^{233}	α^{234}	α^{235}	α^{236}	α^{237}	α^{238}	α^{239}	α^{240}	α^{241}	α^{242}	α^{243}	α^{244}	α^{245}	α^{246}	α^{247}	α^{248}	α^{249}	α^{250}	α^{251}	α^{252}	α^{253}	α^{254}	α^{255}	α^{256}	α^{257}	α^{258}	α^{259}	α^{260}	α^{261}	α^{262}	α^{263}	α^{264}	α^{265}	α^{266}	α^{267}	α^{268}	α^{269}	α^{270}	α^{271}	α^{272}	α^{273}	α^{274}	α^{275}	α^{276}	α^{277}	α^{278}	α^{279
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...IAENLNTAKEIHTTKGTADTALQTFIVKKVDENNADDANAIT-----4223
 ...IAENLNTAKEIHTTKGTADTALQTFIVKK-----DGATDDEIT-----LES-1

VKYDVNVGDGLKIGDDKKIVADITTLIVTGEKVSVIPAGANSWNNKKLVNABGLATALANLS.
VKYDVNVGDGLKIGDDKKIVADITTLIVTGEKVSVIPAGANSWNNKKLVNABGLATALANLS..
VGQKNVANNQ--VNVLTLKGENGILNIKTDKNGIVTFGIN--
VKRDSIQNGEKTVNHLKLKGENGLTVAINKDGI VTFGIN--
* * * * *

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FIG. 28M

WTAKADYADGESEGETDQEVKAGDKVTF-KAGKNLKVQKSEKDFVYSLQD	API
.....	Rd
.....	4223
TTSGLKAGKST-LNDGLSKHPTGSEQIQVGADG	LES-1
.....	
TQSGLKAGDSTTLAKDGKSHKPNASNEQIQVGADG	
* * * * *	* * * *
.....	* * *

TLTGLTSITLGGTANGRNDTGIVINKDGLTITLANGAAAGTDA SNEVT---ISVTKDGISA.
TLTGLTSITLGGTANGRNDTGIVINKDGLTITLANGAAAGTDA SNEVT---ISVTKDGISA.
VKFAKVNNGWGAGIDGTRITRDEIGFTGINGSIDKSKPHL-----SLDGINA.
VKFAKVDK-QNSSTGIDGTSRITKQIGFTGANGSLDTTKPHLTKDKLKVEVEITNGINA...
* * * * *
* * * * *

K9
HSF
API
Rd
4223
LES-1

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FIG. 28N

```

...
GNKETTNNKSA-----LKTYKDTONTA
...
GNKETTNNKSA-----LKTYKDTONTA
...
GKKKTNIQSELAQNSHDAVIGKLYDLKT
...
GKKKTNIQSDITQNSNDAVIGGRVYDLKT
* * * * *

```

GATQPAANTA EVAKQDLVDLITKPATGAAGNGADAKAPDTTAA TVGDLRGLGMWSAKKTAE.

-DE..

EL..

EL..

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[illegible]

FIG. 280

[illegible]

Figure 1. The effect of the concentration of the initiator on the polymerization of α -methylstyrene in the presence of SnCl_4 at 0°C . The concentration of α -methylstyrene was 0.1 mol/L , and the concentration of SnCl_4 was 0.005 mol/L . The polymerization was carried out in CH_2Cl_2 for 24 h. The concentration of the initiator was 0.001 mol/L (○), 0.002 mol/L (□), 0.005 mol/L (△), 0.01 mol/L (◇), and 0.02 mol/L (×).

...DATTCGQVNAD-RGKVK---AEDENGADVDRKV-----
 ...-----
 ...-----
 ...-----
 ...-----
 ...DATTAQGTINAEGRKVVVKSGNGATATETDRKV-----
 ...DATTAQGTINAEGRKVVVKSGNGATATETDRKV-----
 ...QNGQNTITGLSNTLANVTNDKGSVRTTEQGVLIKDEDKTRA
 ...KDGQNTITGLSNTLANVTNDKAGHSLS-QGLAN-DTDKTRA
 ...*
 ...

ININITDSSQNAVGSSTITFKAGNLIKIKQSEN.
ATVKQVAKAINDAATFKVK/ESTDDDIENGAAGKNETTDQALKAGDTLTLKAGKNILKAKLDQ.
ATVKQVAKAINDAATFKVK/ESTDDDIENGAAGKNETTDQALKAGDTLTLKAGKNILKAKLDQ.
...
ATVGDVAKAINDAATFKVKVEN--DQSATIDDSPTDDGANDALKAGDTLTLKAGKNILKVKRDG--
ATVGDVAKAINDAATFKVKVEN--DQSATIDDSPTDDGANDALKAGDTLTLKAGKNILKVKRDG--
...
ASIVDVL SAGFN LQNGEAVDFVSTYDTVAFADQVATTAKVTYDQTSKTSKVVVDVNVDDIT.
ASIGDVLNAGFN LQNGEAVDFVSTYDTVDFIDQVATTAKVTYDQTSKTSKVVVDVNVDDNK.
*** * * * *

FIG.28Q

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-----FALANDLVKNATVSDKLSLGANGKKVDITS DANG-----
D--FTYS.KKE.KNLTVEITE...F...N.....
GKSVT...K.D.TS.K.....I.KDIN.....
GKSVT...K.D.TS.K.....I.KDIN.....
T.EK.....N.....T.....
K.G.T...T.TI.CGAAAGAT.TPKNVTSTTDG
K.SMRT...T.TI.GSTTTGSA.TPKNVTSTASG
-KNIT...S.S.....T.N.N...TK.
-KNIT...S.S.....T.N.N...TK.
N.....T.....
IEVK-DKILGVKTTTITSTIGCANKFALSNOATGDALVKASDIVA--
IEVTSKILGVKTTTITSTIGCANKFALSNOATGDALVKASDIAT--
... * * * *

210 220 230 240 250
LKFAKQGT-NGQNEV--VHLNGTASTLDDPRVGKTAHLTKELSDITERN--RAASVGDVINA...
L.T.NG...S...T.TLA.T.G.VDTN.DAVNH--...Q...S...
L.T.NG...T.TIT.MT.QASNGVAVQ-NH--...A...
L.T.NG...T.TIT.MT.QASNGVAVQ-NH--...A...
PS...T.TIT.TKSAINGVDVQNH--...A...
DAA--A.DIT...G...T.TK.SPAT.IDGDDQS.HYT--...IK...
V.GA.GANGDIT--TN...Q.TLNGVWSKLDGNGITADEKK...Q...S...
DSKT--DDA--I...T.TLNGGATTNLGNGITNEKK...K...
X.DSKT--DDA--I...T.TLNGGATTNLGNGITNEKK...K...
P...--

FIG. 28R

FIG. 28R

.....TLSCDIQTAKGASQANNSAGYVDADGNKVIYDSTDKYQA...
TLSCDIQTAKGASQASSASGYVDADGNKVIYDSTDKYQV...
 * *** ** *** * * * * *
 ...260 270 280 290 300
 ...GNIRCAK--TIGG-TVNDVFSYDVEFASGANVSVTTDIN--
Q.NGNVDFVR.Y.T...N-----A.TAH-
Q.NGASVDFVNAY.T...N-----T.T.N...TAH-
Q.NGASVDFVNAY.T...N-----T.T.N...TAH-
Q.NGAS-----N...D.VN.L.T.N...TAHN
K.V.AGSTIT-QQSE...H...L...DTEITTV.V.S--
K.V.TGAT---S...R...L...SEETTL.V.S--
V.V.PASANNQ-E.I...A...D.V.DKDTT.VES--
V.V.PASANNQ-E.I...A...D.V.DKDTT.VES--
KNDGTVD.TKEVAKDKLVAQAQTPDGTILAQMNKSVI.KEQVN.A.--
NDKGQVD.NKEVAKDKLVAQAQTPDGTILAQMNKSVI.KEQVN.A.--
 ...

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310 320 330 340 350 360 ...
 KKTIVRVDVTGLPVQVVTEDSKTVKVGNEYEAKQDSADNDKVV-ENGKLAKTIVKLVSA...
G.....K.D....NQ...E...
G.....D.K.....E...
G.....D.K.....E...
GE...
F.....G.....K.E.V...

115 777 29992462

FIG.28S

.ENCK.TE.KIGAKTS.IKEKCKLFT.KANK.TNKVDG.NATEDA-DE..GLV.AKDVID....
ESNGKSTK.KIGAKTSIGIKEKCKLFT.KANKOIN.VASNNAAADD-DE..GLV.AETVIN....
.DNCK.TE.KIGAKTS.IK.HNGKLT.K.LKD.NNN.VTVTETDGKOE.NGLV.AKAVID....
.DNCK.TE.KIGAKTS.IK.HNGKLT.K.LKD.NNN.VTVTETDGKOE.NGLV.AKAVID....
.....
..QGINEINAFVKGLEKAASDNKTKNAAVTVGDINAVAQPLTFAG-DT.TT..KLGETLTI...
..QGINEINAFIKGLENAAKDITKNAAVTVGDINAVAQPLTFAG-DT.TT..KLGETLTI...
** *

... 370 380 390 400
...NGINPVKISNADGTEDTDAVSFKQKALQDKQVILSAS
...S.....T.
...S.Q.....E..EN.....E.....T..
...S.Q.....E..EN.....E.....T..
.....N.....
.....E.....N.....
...VNKTGMR.KTIDANGQNG.---FATVASGINVTF---
...VNKAGMR.KTTCANNQAGQ---FEIVTSGINVTF---.D
...VNKAGMRVKTTCANGQND.---FATVASGINVTF---.D
...VNKAGMRVKTTCANGQND.---FATVASGINVTF---.D
.....
...KGGQTDINKLTNNIGVAGTDGFTV.LAK.LTNLN.VN
...KGGQTDINKLTNNIGVAGTDGFTV.LAK.LTNLN.VN
...

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LESS-1

FIG. 28T

FIG. 28T

NAYANGSDADGKGATQITLGNLNFKEFKSTDSSELNKAAGDITVTFPKGVSQVGGDKAT...
...T.N.....S.G.....S.G..K.S.T.....S..
...N.....N.G.....G.....VEN.....E..
...N.....N.G.....G.....VEN.....E..
...GI...S.G.....G.....EN..
...V.V.....S.G.....G.....DK...I..
GNGTTATVING-TDGIIVKYDAKVGDLKLDG-KIAADTTALTIVNDGNANPKGVADVA..
GNGTTAVTGDATNGITVKEAKVGDLKIGNDQKITADTTALTIVTGK-----VTAPD..
GNGTTAEVTKANDGSIIVKYNKVADGLKLDG-KIVADITVLTIVADGK-----VTAPN..
GNGTTAEVTKANDGSIIVKYNKVADGLKLDG-KIVADITVLTIVADGK-----VTAPN..
...G...S.G.....G.....EN..
AGGTIKIDDKGVSF-----
AGGTIRIDEXGISFVDANGQAKANTPVLSANGLDLGKRIISNIGAAVDDINDAVNFKQFNEVAK...
* * *

... 470 480 490 500
...IQDCAKTTTGLVEASELVDLSNKLGMKVGVGKDGTC---AT
...SK.N.E.....E.....E.V.S.---EL
...N.T...D.....E.....D.S.---EL
...N.T...D.....E.....D.S.---E..
...T.T.....V..
...STDEK---T.KG..TA..S.S.TTTAAEADG.---TL
...ATNGKK---N.G.A.A...S.TAK-AEADTANGGEL
...NGDGKK---F.D.G.A.A...S.TATA..E.---EV
...NGDGKK---F.D.G.A.A...S.TATA..E.---EV

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11
K9
HSF
API

No.	a		b		c		d		e		f		g		h		i		j		k		l		m		n		o		p		q		r		s		t		u		v		w		x		y		z	
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50		
1	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50		
2	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50		
3	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50		
4	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50		
5	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50		
6	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50		
7	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50		
8	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50		
9	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21																															

FIG. 28U

	510	520	530	540	550	560 ...
DCGTHD-TLVKSGDKVTLKAGDNLKVKQEGINFYVLDELITGVKSVEFKJENGANGASTK...						
SKE-	A.K.					A.
ASNE-	E.	D.				A.S.
ASNE-	E.	D.				A.S.
-	A.K.	D.				A.
NASE-QE.A.	F.K.	A.	S.Q.A.	LT.ITLIGN.	K---	E.
ADE-KE.A.ET.F.K.	A.	S.Q.A.	LT.ITLIGN.	K---	E.	
PANSAGQE.A.	F.	I.S.KD.	S.KK.	KDLT.	ANG.TCSE.	
PANSAGQE.A.	F.	I.S.KD.	S.KK.	KDLT.	ANG.TCSE.	
-						
-						
K7YH--					ANGVP.	
*					* * *	
	570	580	590	600		
... ITKDGLTITTPAND-ANGAAATDADKIK----	VASDGISAGENKAV					
... L.G....TV						
... S.G----						
... S.G----						

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FIG.28V

M4071
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K9
HSF
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4223
LES-1

TTTTT 29E9E6E0

.....G- GA.G.NT.NT.S---.TK.....
.....R.SG-.....
.....N.....G---G.NN.NT.S---.TK.....DQS.
.....N.....G---G.NN.NT.S---.TK.....DQS.
.....G- GA.G.NT.NT.S---.TK.....
.....G- GA.G.NT.NT.S---.TK.....
.....F.....R.....
.....VD...KP..D.DKL..L..HGKPLDACHQV...L.-GNSD-.I
.....* *** * * * * ** * * * *

610 620 630 640 650 660 ...
KNVWSGLKFGDANFNPLTSSADNLTKQYDNAYKGLJNLDEKSKGKQPTVADNTAATVGD...
.....D.....GAD...L.....
.....D.....GAD...L.....
.....D.....
.....D.....N.D.....GTD...V.....
.....D.....GAD...L.....
T.....GHTLANGIV..FE-H.....D.....GADNN-
T.....GHTLANGIV..FE-H.....XD.....GADNN-
.....
.....
.....TLTNIKSTLP.I.TPNT.NA.AGQAQSLPISLSAAQSN..S.K.V...

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[illegible]

FIG. 28W

33
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K22
M4071
12
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K9
HSF
API
Rd
4223
LES-1

```

      *   **   *   *   *   *   *   *   *   *   *   *
      ...    670    680    690    700
...TGLGMWISADKTTGES-KEYSAQVRNANEVKFKSGNGIN
-----
      *   **   *   *   *   *   *   *   *   *   *
      ...    670    680    690    700
...LN. N. . . . . H
...LN. N. . . . . H
...K. LN. N. . . . .
-----
      *   **   *   *   *   *   *   *   *   *   *
      ...    670    680    690    700
...G.-T. HD.
...LD. N.
...PNQ. N.
...PNQ. N.
-----
      *   **   *   *   *   *   *   *   *   *   *
      ...    670    680    690    700
...LNV.FNLQTNHNQVDF.V.A.DIVNFVNGTGADITSVRSR
*** * * * *

```

710	720	730	740	750	760	...
VSKTLNGTRETTEFLANDENALAFGSGKALRINTVAIGTNVNAEKSGAPGDNYIED...						

V-..R.....Y.						

V-..R.....Y.						
.....						

.....						

V-..R.....G.						
.....						

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FIG. 28X

FIG. 28X

V- R. G.
V. G.
V. G.

DGTMENITVNTALATDDDCNVL. KAKD. KFYKA. DLMFN. SILKAGKSADAKTPTGLSLVN. . .

*** ** * * * * *
770 780 790 800

KAGGSYAFENDNRITTSKNTFVLGNKAKYKANGKVDI

...

...

...

...

S. RD. N. L. EE

...

...

...

...

...

...

...

FNA. KGST. DAVALNLSKA. FKSOGTTTTVSSDGSIQK

...

...

...

...

...

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K22
M4071
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K9
HSF
API
Rd
4223
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FIG. 28Y

[illegible]

VWKSNEFTVKNADGETSLVKVGDLYYYSKEDI DLITGQPKLDGNIVAAKYQDKCKVWS-V.
VWKSNEFTVKNADGETSLVKVGDLYYYSKEDI DPATGKPVTNGNVA/AKYQDKCKVWSAD..
VWKSNEFTVKNADSETNLVKVGDLYYYSKEDI DPATSKPMTGKITE---- KYKVENGKAVSAN
VWKSNEFTVKNADSETNLVKVGDLYYYSKEDI DPATSKPMTGKITE---- KYKVENGKAVSAN!
VDSSGOAKANTPVLSANGLDLCGGKVISNVKGTKTDIDAANVOQLNEVRNLLGLENAEIDNAD...
DNSSI-----T!SKDGLNVCGKVISNVKGTKTDIDAANVOQLNEVRNLLGLENAEIDNAD... * + * + *

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K22
M4071
12
11
K9
HSF
API
Rd
4223
LES-1

..TTNTEATITNKGSGVVTGNQ-----
 ..GSSNTAVTLTNKGYVVTGNQ-----
 ..GSK-TEVTLTNKSGSVVTGNQ-----
 ..GSK-TEVTLTNKSGSVVTGNQ-----
 ..-----
 ..GNGVNIADIKDPNCGSSSNRTVIKAGTIVLGCKGNNDT
 ..GNGVNIADIKDPNCGSSSNRTVIKAGTIVLGCKGNNDT

FIG. 28Z

FIG. 28Z

...

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API
Rd
4223
LES-1

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K22
M4071

	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99
0	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99

FIG. 28A'

VESTDANGDKVTTTFVKTDVELPLTQIYNTDANKKI--V
.....
NEQGIRFFHHNDGNQEPFWQGRNGIDSSASGKHSAVATGFQ-
.....
NEQGIRFFHHNDGNQEPFWQGRNGIDSSASGKHSAVATGFQ-
.....

KDCQTKWYELNADGTADMTKEVTLGNVSDGKKVKNDG---KWHAKADGTADTKTGEVD.
 KNGD-KWYTKDDGSTDMTKEVTLGNVSDGKKVKEDN----KWYGVKSDGSTDKTQVVEE.
 KKADGKWYELNADGTASN-KEVTLGNVDANGKKVKV/TENGADKWYTYTNADGAADTKGEVS.
 KKADGKWYELNADGTASN-KEVTLGNVDANGKKVKV/TENGADKWYTYTNADGAADTKGEVS.
 AKADGEAAVAIGRQTQACNQSIAGUNAQATGDSIAIGTGNVAGKHSGAIGDPSTVKADN..
 AKADGEAAVAIGRQTQACNQSIAGUNAQATGDSIAIGTGNVVTGKHSGAIGDPSTVKADN..
 ** * * * * * * * * * *

FIG. 28B,

12
11
K9
HSF
API
Rd
4223
LES-1

[illegible]

```

810      ETVTWKDKGKETTIVPKALGAIVNSVYLGNKSTATOKERNLKSDDGTAGATTIAGTIGI...    860 ...
.....
820      EXE.VG..AK.K..Q..E..A....A....A....
.....
830      .....
.....
840      .....
.....
850      .....
.....
860      VTESNSVAL.SNSAISAGTHA.TQAK-----T...A....
.....
870      VTESNSVAL.SNSAISAGTHA.TQAK-----T...A....
            *   *   *   *   *****
            ..       870        880        890        900
            .... VNGFACATAHCAVSVCASGEERRIONVAAGEISAISSID
            ....                               ---K....
            ....

```

33 32 29

K22
M4071
12
11
K9
HSF
API
Rd
4223
LES-1

[illegible]

FIG. 28C,

```

910      920      930      940      950      ...
AINGSOLYAVAKGVINLAGOVN-----KVKKRADAGTASALAAASQLPQASWCKSWSLA...
.....NLEKVN.....T.P.....
.....P.....
.....P.....
.....P.....
.....P.....
.....P.....
.....NLEKVN.....T.P.....A.....
.....NLEKVN.....T.P.....
.....NLEKVN.....T.P.....A.....
.....NLEKVN.....T.P.....A.....
.....P.....
V.....ATQSI NAT.ELDHRIHQENK.N. IS. M.MASM. YIP.R. TGG...
V.....ATQGI NAT.ELDHRIHQENK.N. IS. M.MASM. YIP.R. TGG...
***** ** ** *
***** ***** * **** ***** *

```

SEQ	ID	NO:56
SEQ	ID	NO:55
SEQ	ID	NO:59
SEQ	ID	NO:58
SEQ	ID	NO:57

SEQ	ID	NO	59
SEQ	ID	NO	58
SEQ	ID	NO	57

FIG. 28D;

...	960	970	980	990	1000
...	GSSYQOQSGLAIGVSRISDNKVI	IRLSGTINSQKGTGVAAGVGQW*			33
...	N.....	N.....			32
...	N.....	N.....			29
...	N.....	N.....			K22
...	N.....	N.....			M4071
...	L.....	L.....			12
...	N.....	N.....			11
...	N.....	N.....			K9
...	N.....	N.....			HSF
...	N.....	N.....			API
...	N.....	N.....			Rd
...	IATHN. GAV. V. L. KL.	QWVFKIN. SADT. .	HV. A. V. A. FHF*		4223
...	IATHN. GAV. V. L. KL.	QWVFKIN. SADT. .	HV. A. V. A. FHF*		LFS-1
...	*****	*****	* ** *****	* * * * *	

FIG. 29

Oligonucleotides primers to PCR amplify truncated strain 11 S44 hia gene.

Node I

5' CCGATTCATATGTCGCAACGGTCTGGCGAACACCAACT 3' 6817 SL

sty I

H T I T F A L A K D L G
 CACACATTACCTTTCTCTTAGCGAAGAACTTGGT
 GIGIGTAATGGAACGAAATCGCTTTCTGTGGAACCACTTAGGGC
 3' 5' 6818.SL

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FIG. 30A

Construction of JB-2930-3, pBR T7/S44 hia(11)/cer/kanR

PCR amplify Nde-Sty S44 hia (11)
clone into pCR II

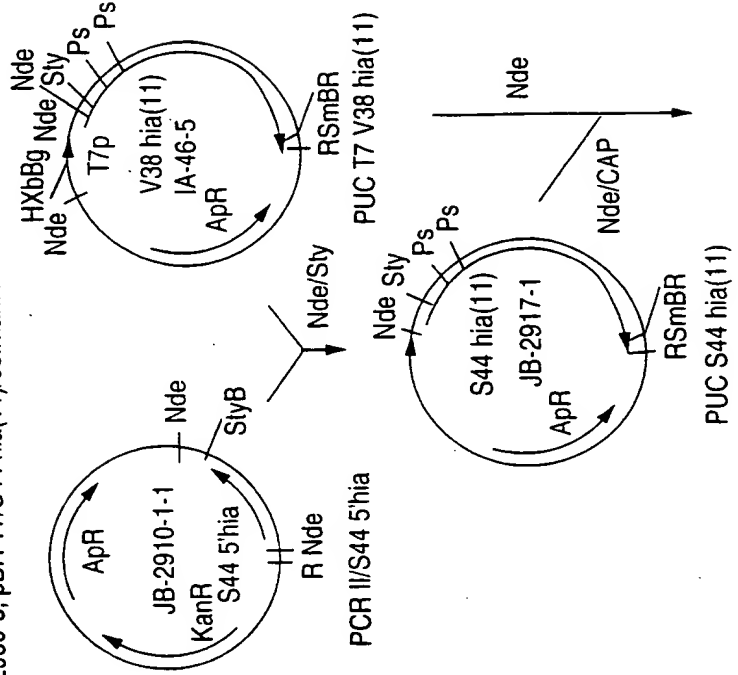


FIG. 30A

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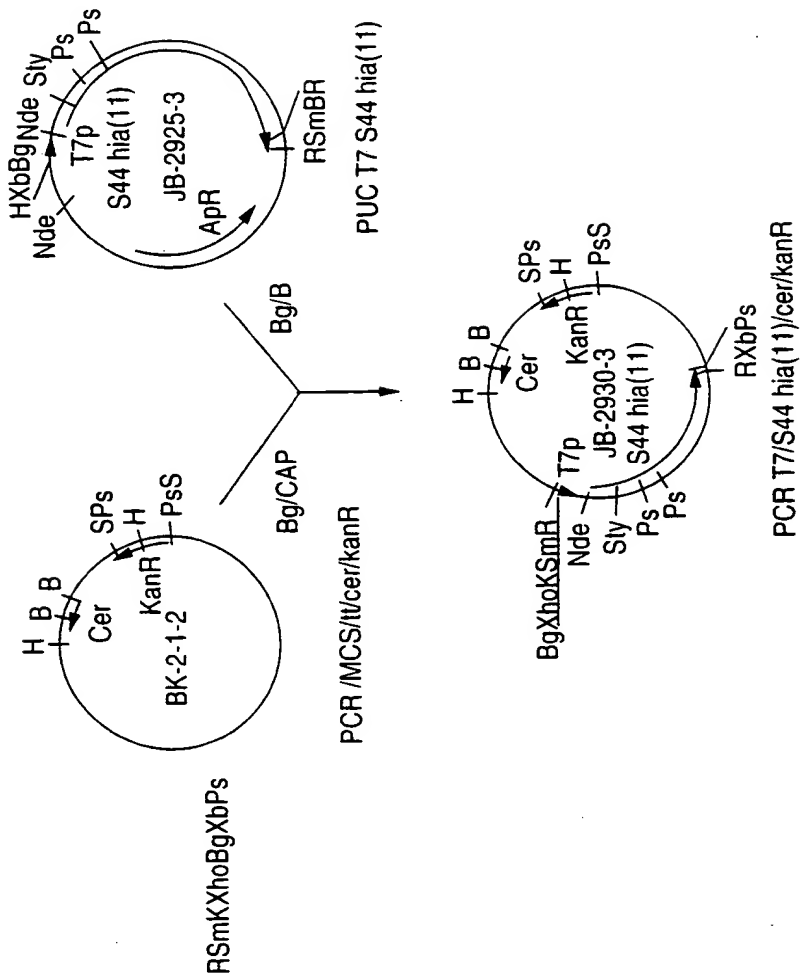


FIG.30B

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Production of S44 rHia from different vectors

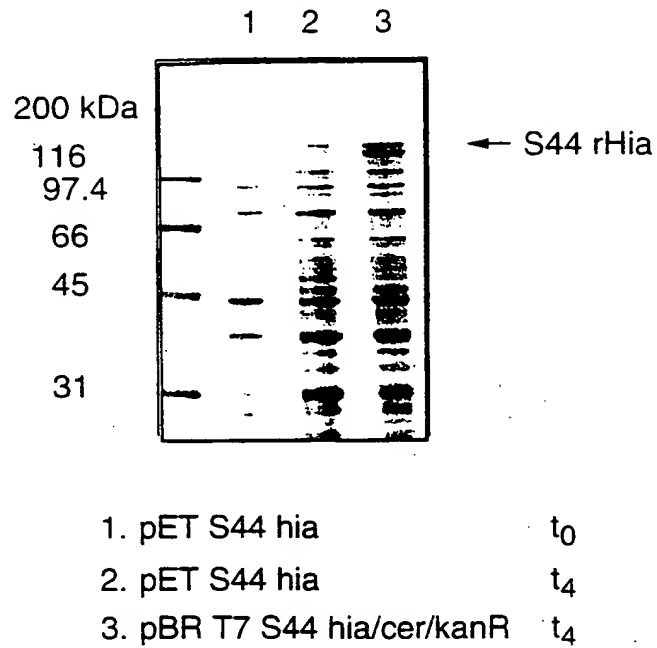


FIG.31

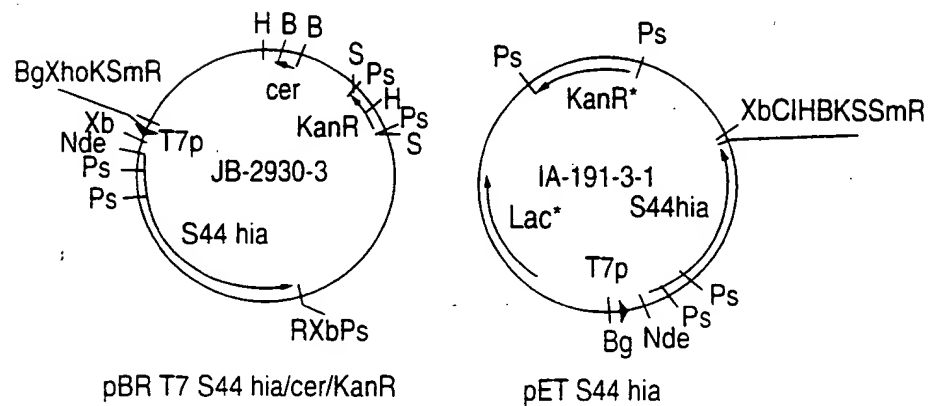


FIG.32